

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 04:17:29 ; Search time 2848.01 Seconds
(without alignments)
9405.294 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	8						Description
	No.	Score	Query Match	Length	DB	ID	
	1	674	75.1	805	12	BI918620	BI918620 603176570
	2	565.6	63.1	1047	12	BM914622	BM914622 AGENCOURT
c	3	467.2	52.1	1041	12	BI412864	BI412864 602988202
	4	467	52.1	524	13	BX281777	BX281777 BX281777
	5	408.2	45.5	549	9	AA706226	AA706226 ah28a07.s
	6	396.6	44.2	412	9	AI041451	AI041451 ow36c02.s
	7	363.8	40.6	427	10	BF108794	BF108794 7152g03.x
	8	318.6	35.5	488	13	BX529505	BX529505 BX529505
c	9	255	28.4	949	12	BI410828	BI410828 602963734
	10	234.4	26.1	333	10	BE983573	BE983573 UI-M-CG0p
	11	224	25.0	297	9	AA772412	AA772412 ai44e12.s
	12	210.2	23.4	795	12	BI651936	BI651936 603298677
	13	195.2	21.8	259	10	BE648780	BE648780 UI-M-BH2.
	14	195.2	21.8	327	9	AA968077	AA968077 uh09h01.r
c	15	182.6	20.4	362	13	BX089049	BX089049 BX089049
	16	169.8	18.9	529	10	AW476657	AW476657 uq79e01.y
c	17	154.8	17.3	539	9	AL918370	AL918370 AL918370
	18	142	15.8	657	13	BQ078813	BQ078813 fy81c06.y
	19	111	12.4	256	10	AW762061	AW762061 ur53c01.y
	20	107.6	12.0	458	9	AI152190	AI152190 ud18h10.r
	21	105.2	11.7	750	28	BZ847665	BZ847665 CH240_239
	22	101	11.3	493	28	BH057870	BH057870 RPCI-24-9
c	23	100.4	11.2	481	28	AZ987593	AZ987593 2M0270P10
c	24	97.4	10.9	180	29	CE103297	CE103297 tigr-gss-
	25	90.2	10.1	243	10	BB570162	BB570162 BB570162
c	26	85	9.5	512	9	AI073386	AI073386 ool3d06.x
	27	81.2	9.1	167	9	AI836531	AI836531 UI-M-AP0-
	28	76.6	8.5	477	10	BE984041	BE984041 UI-M-CG0p
	29	70.8	7.9	761	13	BX876483	BX876483 BX876483
	30	67.2	7.5	765	12	BI522417	BI522417 603175321
	31	67	7.5	769	12	BI413085	BI413085 602990205
	32	66	7.4	751	29	CNS04J6G	AL293137 Tetraodon
	33	64.8	7.2	321	10	BE983721	BE983721 UI-M-CG0p
	34	64.4	7.2	538	9	AL925790	AL925790 AL925790
c	35	61	6.8	491	9	AL909688	AL909688 AL909688
c	36	60.2	6.7	322	9	AL909689	AL909689 AL909689
	37	59	6.6	356	29	CG614660	CG614660 OST303096
	38	58.8	6.6	363	29	CE326275	CE326275 tigr-gss-
	39	58.8	6.6	413	14	N62228	N62228 yz63c08.s1
	40	58.4	6.5	685	14	CA351220	CA351220 622234 NC
	41	53	5.9	1630	11	AK051824	AK051824 Mus muscu
	42	51.6	5.8	925	29	CNS0091P	AL053013 Drosophil
c	43	51.6	5.8	982	13	BX415111	BX415111 BX415111
	44	50.8	5.7	647	12	BI960178	BI960178 HVSMEn002
	45	50.4	5.6	251	9	AW045376	AW045376 UI-M-BH1-

ALIGNMENTS

RESULT 1
BI918620
LOCUS BI918620 805 bp mRNA linear EST 16-OCT-2001
DEFINITION 603176570F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240969 5',
mRNA sequence.
ACCESSION BI918620
VERSION BI918620.1 GI:16182295
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 805)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11607 row: k column: 18
High quality sequence start: 2
High quality sequence stop: 778.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240969"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 75.1%; Score 674; DB 12; Length 805;
Best Local Similarity 98.7%; Pred. No. 2.8e-127;
Matches 732; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGC-TTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTG 59
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 Db 64 ATGAGGCGCGACCCGGCCCCCGGCGTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTG 123
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 Qy 60 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGGA 119
 |||
 Db 124 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGGA 183
 |||
 Qy 120 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 179
 |||
 Db 184 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 243
 |||
 Qy 180 GCCCGCCTCGGGTTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 239
 |||
 Db 244 GCCCGCCTCGGGTTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 303
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 Qy 240 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 299
 |||
 Db 304 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 363
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 Qy 300 GCGCTACATCTTTTTCTGGAGCCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTG- 358
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 Db 364 GCGCTACATCTTTTTCTGGAGCCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGT 423
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 Qy 359 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 418
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 Db 424 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 483
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 Qy 419 ACTGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGA 478
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 Db 484 ACTGCGCCACCCGGCCCCAAGTTGAAGAAGATGACGAGCCAGACGGGACAGGTGGGTGAGA 543
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 Qy 479 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCA 538
 |||
 Db 544 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCA 603
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 Qy 539 AGGATGGCAAGGAGCTCAACCG-CAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 597
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 Db 604 AGGATGGCAAGGAGCTCAACCGTCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 663
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 Qy 598 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGA-GTATGTCTG 656
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 Db 664 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGGTATGTCTG 723
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 Qy 657 CGAGG-CCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCG 715
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 Db 724 CGAGGCCCAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGTTTTACGTCAACAGGT 783
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 Qy 716 TGAGCACCAACCTGTCATCCTG 737
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 Db 784 TGAGCACCAACCTGTCATCCTG 805

RESULT 2

BM914622

LOCUS BM914622 1047 bp mRNA linear EST 12-MAR-2002

DEFINITION AGENCOURT_6615334 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480308

5', mRNA sequence.

ACCESSION BM914622

VERSION BM914622.1 GI:19365001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1047)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2002 row: p column: 05
High quality sequence stop: 541.

FEATURES
source Location/Qualifiers
1. .1047
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480308"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 63.1%; Score 565.6; DB 12; Length 1047;
Best Local Similarity 96.8%; Pred. No. 4.4e-105;
Matches 577; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy	272	GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTTCCTGGAGCCCACGGAAC	331
Db	1	GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTTCCTGGAGCCCACGGAAC	60
Qy	332	AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGA	391
Db	61	AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGA	120
Qy	392	AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA	451
Db	121	AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA	180

QY 452 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGTA 511
 |||
 Db 181 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGTA 240
 |||
 QY 512 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 571
 |||
 Db 241 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 300
 |||
 QY 572 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 631
 |||
 Db 301 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 360
 |||
 QY 632 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 691
 |||
 Db 361 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 420
 |||
 QY 692 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAGCCCC 751
 |||
 Db 421 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAGCCCC 480
 |||
 QY 752 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCG 811
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 Db 481 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGCCTGCTACTACATCG 540
 |||
 QY 812 AGGGCATCAACCAGCTCTCCTGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGT 867
 |||
 Db 541 AGGCCATCAATCAGCTTTCCTGCAAATGTCCCAATGGATTCTTCCGACCAACATGT 596
 |||

RESULT 3

BI412864/c

LOCUS BI412864 1041 bp mRNA linear EST 14-AUG-2001
 DEFINITION 602988202F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5144016 5',
 mRNA sequence.

ACCESSION BI412864

VERSION BI412864.1 GI:15173787

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1041)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11355 row: d column: 01

High quality sequence start: 11

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FEATURES             Location/Qualifiers
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                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="Czech II"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:5144016"
                        /tissue_type="pooled lung tumors"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NCI_CGAP_Lu33"
                        /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCCGCCTCTGTTTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

Query Match 52.1%; Score 467.2; DB 12; Length 1041;
Best Local Similarity 86.6%; Pred. No. 5.7e-85;
Matches 563; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

Qy	165	CAGCACCCGAGAGCCGCCCGCCTCGGGTCGGGT-----GGCGTTGGTAAAGGTGCTGGACA	220
Db	656	CACCTCGAGATGCCCGCCCGCCTCGGGTTCGGTTGGCGTCTTGGTGAAAGGTGCTGGACA	597
Qy	221	AGTGGCCG--CTCCGAGCGGGGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTG	278
Db	596	AGTTGCCGGCTCCCGGATCGGGGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTG	537
Qy	279	TGTGCCGCTCGAAAGGAACCAGCGCTACATCTT-TTTCCTGGAGCCCACGGAACAGCCCT	337
Db	536	TGCGCCGCTCGAAAGGAACCAGCGCTACATCTTGTTCCTGGAGCCCACCGAGCAGCCCT	477
Qy	338	TAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGG	397
Db	476	TAGTTTTTAAGACAGCCTTTTGCCCCGGTCGACCCTACGGCAAATACATCAAGAAAGAGG	417
Qy	398	TGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGGCCAAGTTGAAGAAGATGAAGAGCC	457
Db	416	TGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGGCCAAGCTGAAGAAGATGAAGAGCC	357
Qy	458	AGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCC	517
Db	356	AGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCAAGTGTGAGGCAGCGCGGGAAACCCCC	297
Qy	518	AGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGA	577
Db	296	AGCCCTCCTATCGCTGGTTCAAGGATGGCAAGGAATCAACCGGAGTCGTGATATTTCGA	237
Qy	578	TCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGG	637

Db	236	TCAAGTATGGCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAGTGAGGGTGGAGG	177
Qy	638	ACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGGCC	697
Db	176	ATGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCGTGAGGGGCC	117
Qy	698	GGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGT	757
Db	116	GACTCCATGTCAACAGCGTGAGCACCCTCTGTATCCTGGTCGGGCATGCCCGGAAGT	57
Qy	758	GCAACGAGACAGCCAAGTCCTA--TTGCGTCAATGGAGGCGTCTGCTACT	805
Db	56	GCAATGAGACCGCCAAGTCCTACCATGTGTGAATGGAGGCGTGTGCTACT	7

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FEATURES
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                /mol_type="mRNA"
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                /clone="IMAGp998K1811607 ; IMAGE:5240969"
                /lab_host="DH10B"
                /clone_lib="NIH_MGC_121"
                /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

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Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 52.1%; Score 467; DB 13; Length 524;
 Best Local Similarity 100.0%; Pred. No. 4.7e-85;
 Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
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Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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Db     118 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 177

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db     178 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 237

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db     238 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 297

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db     298 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 357

Qy     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db     358 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 417

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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Db     418 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 477

Qy     421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 467
          |||
Db     478 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 524
  
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RESULT 5

AA706226

LOCUS AA706226 549 bp mRNA linear EST 12-JAN-1999
 DEFINITION ah28a07.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
 1240116 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR
 NDF04 ;, mRNA sequence.

ACCESSION AA706226

VERSION AA706226.1 GI:2716144

KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyT not found
 Insert Length: 689 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 451.

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="1240116"
 /tissue_type="parathyroid tumor"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_parathyroid_tumor_NbHPA"
 /note="Organ: parathyroid gland; Vector: pT7T3D
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGACCAATTTTTTTTTTTTTTTTTTTT
 TTTT-3'], double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,
 NIH."

ORIGIN

Query Match 45.5%; Score 408.2; DB 9; Length 549;
 Best Local Similarity 91.7%; Pred. No. 5e-73;
 Matches 431; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
 |||
 Db 15 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 74

QY	484	TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT	543
Db	75	TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT	134
QY	544	GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAAC	603
Db	135	GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAAC	194
QY	604	TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC	663
Db	195	TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC	254
QY	664	GAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACC	723
Db	255	GAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACC	314
QY	724	ACCCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGC	783
Db	315	ACCCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGC	374
QY	784	GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTT	843
Db	375	GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGGACCTT	434
QY	844	GTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC	893
Db	435	GGGCTGCACTGCTTAGAACTTGGTACCCAGAGCCACCACTTCCCCATCTC	484

RESULT 6

AI041451

LOCUS AI041451 412 bp mRNA linear EST 28-AUG-1998

DEFINITION ow36c02.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone

IMAGE:1648898 3' similar to TR:O14511 O14511 NTAK : mRNA

sequence.

VERSION AI041451.1 GI:3280645

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM *Homo sapiens*

Eukaryota: Metazoa: Chordata: Gymnophiona: Amphisbaenidae: *Amphisbaena*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Artiodactyla; Cetartiodactyla

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 412)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bente, Seeger, Ph.D., M. Bente

CDM Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library: Accession # F01111

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 671 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1. .412

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1648898"

/tissue_type="parathyroid tumor"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares_parathyroid_tumor_NbHPA"

/note="Organ: parathyroid gland; Vector: pT7T3D

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGGAGCGGCCGACCAATTTTTTTTTTTTTTTTTTTT
 TTTT-3'], double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,
 NIH."

ORIGIN

Query Match 44.2%; Score 396.6; DB 9; Length 412;

Best Local Similarity 97.6%; Pred. No. 1e-70;

Matches 402; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	426	CACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	485
Db	1	CACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	60
QY	486	GCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGG	545
Db	61	GCTGAAGTGTGAGGCAGCAGCGATAAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGG	120
QY	546	CAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTC	605
Db	121	CAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTC	180
QY	606	ACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	665
Db	181	ACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	240
QY	666	GAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCAC	725
Db	241	GAACATCCTGGGGAAGGACACCGTACGAGGCCGGCTTTACGTCAACAGCGTGAGCACCAC	300
QY	726	CCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGT	785

Db 301 CCTGTCATCCTGGTCGGGGCACGCCGGGAAGTGCAACGNGACAGCCAAGTCCTATTGCGT 360

QY 786 CAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAG 837
 |||

Db 361 CAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAG 412

RESULT 7

BF108794

LOCUS BF108794 427 bp mRNA linear EST 20-OCT-2000
 DEFINITION 7152g03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:3525292 3' similar to SW:NTAK_HUMAN O14511 NTAK PROTEIN
 ;contains MSR1.t1 MSR1 repetitive element ;, mRNA sequence.

ACCESSION BF108794

VERSION BF108794.1 GI:10938484

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 427)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 396.

FEATURES

source

Location/Qualifiers

1. .427

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3525292"

/lab_host="DH10B"

/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and cloneIDs: Soares NbHSF pool 1:
 309384-310919, 323208-325895 Soares Nb2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.6%; Score 363.8; DB 10; Length 427;
 Best Local Similarity 91.3%; Pred. No. 5.4e-64;
 Matches 386; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | | | | | | | | | | |
Db      5 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 64

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      65 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 124

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      125 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 184

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||||
Db      185 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 244

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      245 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 304

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      305 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 364

Qy      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 782
      |||||
Db      365 CACCCTGTCATCCTGGTTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 424

Qy      783 CGT 785
      |||
Db      425 CGT 427
  
```

RESULT 8

BX529505

LOCUS BX529505 488 bp mRNA linear EST 27-JUN-2003

DEFINITION BX529505 NCI CGAP Mam3 Mus musculus cDNA clone IMAGp998N017639 ;
 IMAGE:3153984, mRNA sequence.

ACCESSION BX529505

VERSION BX529505.1 GI:32297863

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 488)

AUTHORS Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
 and Korn,B.

TITLE Mouse UnigeneSet - RZPD2

JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

Db 301 ||||| 360
 GCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTC 360
 QY 829 TCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 Db 361 ||||| 405
 TCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAG 405

RESULT 9
 BI410828/c
 LOCUS BI410828 949 bp mRNA linear EST 14-AUG-2001
 DEFINITION 602963734F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119065 5',
 mRNA sequence.
 ACCESSION BI410828
 VERSION BI410828.1 GI:15171751
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11290 row: d column: 10
 High quality sequence start: 28
 High quality sequence stop: 919.
 FEATURES
 source Location/Qualifiers
 1. .949
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:5119065"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Lu33"
 /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
 strand cDNA was prepared from mRNA obtained from pooled
 lung tumors with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCCTCTGTTTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not
 I and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 28.4%; Score 255; DB 12; Length 949;
 Best Local Similarity 80.0%; Pred. No. 1.3e-41;
 Matches 388; Conservative 0; Mismatches 85; Indels 12; Gaps 7;

QY	397	GTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGC	456
Db	947	GTGGGCCAGATCCTGGGCACTG-CTGCGCCACCCGCCCAA-CTGAAGAAGATGAAGA-C	891
QY	457	CAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCC	516
Db	890	CAAACCAGAAGAGTCGGTGAGAACAGTTCGCTCAAGTGTGAGGCACGGCCGGGGAAACCC	831
QY	517	CAGCCTTCCTACC-----GTTGGTTCAAGGATGGC-AAGGAGCTCAACCGCAGCCGAGAC	570
Db	830	CCCCACCCCTCCCTATCGCTGGTTTCAAGGATGGCAAAGGAAGTCAACCGGAGTCGTGAT	771
QY	571	ATTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAG	630
Db	770	ATTCGCATCAAGTATGCCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAAGTGAG	711
QY	631	GT--GGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCG	688
Db	710	GTTGGAGGATTGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGGAAGGACACCG	651
QY	689	TCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACG	748
Db	650	T-GAGGGCCGACTCCATGTCAACAGCGTGAGCACCCTCTGTCATCCTGGTCGGGGACATG	592
QY	749	CCCGGAAGTGCAACGAGACAGCCAAGTCTTATGCGTCAATGGAGGCGTCTGCTACTACA	808
Db	591	CCCGGAAGTGCAATGAGACCGCCAAGTCTACTGTGTGAATGGAGGCGTGTGCTACTACA	532
QY	809	TCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTC	868
Db	531	TCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTT	472
QY	869	AGCAG	873
Db	471	TGGAG	467

RESULT 10
 BE983573
 LOCUS BE983573 333 bp mRNA linear EST 29-APR-2002
 DEFINITION UI-M-CG0p-bgi-c-07-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 UI-M-CG0p-bgi-c-07-0-UI 3', mRNA sequence.
 ACCESSION BE983573
 VERSION BE983573.1 GI:10654893
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 333)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine The following repetitive elements were found in this cDNA sequence: 15-105,
>GC_rich#Low_complexity
Seq primer: M13 Forward
POLYA=No.

FEATURES

source Location/Qualifiers

1. .333

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-CG0p-bgi-c-07-0-UI"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH_BMAP_Ret4_S2"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine

TAG_SEQ=None found"

ORIGIN

Query Match 26.1%; Score 234.4; DB 10; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.3e-37;
Matches 241; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTCGCTCGCCTGC 60
|||||

Db 82 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 141

QY 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
|||||

Db 142 TACTCGCCCAGCCTCAAGTCGGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 201

QY 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||||
 Db 202 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCG 261
 QY 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||||
 Db 262 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 321
 QY 241 GGGCTGCAGCGC 252
 |||||
 Db 322 GGGCTGCAGCGC 333

RESULT 11

AA772412

LOCUS AA772412 297 bp mRNA linear EST 31-DEC-1998

DEFINITION ai44e12.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
 1359886 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR
 NDF04 ;, mRNA sequence.

ACCESSION AA772412

VERSION AA772412.1 GI:2824195

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 297)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

Insert Length: 667 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 267.

FEATURES

source

Location/Qualifiers

1. .297

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="1359886"

/tissue_type="parathyroid tumor"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares_parathyroid_tumor_NbHPA"

[note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenoma was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."

ORIGIN

```

Query Match      25.0%; Score 224; DB 9; Length 297;
Best Local Similarity 92.2%; Pred. No. 1.7e-35;
Matches 236; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY       405 GATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGG 464
           ||||| |   | |   |         | ||| | |||||||||||||||||||||||||
Db        42 GAGCCCGATCCCGGGAGAAAGCCACCCGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGG 101

QY       465 ACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTC 524
           ||||||||||||||||||||||||||||||||||||||| | |||||||||||||
Db       102 ACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCGGTGAATCCCCAGCCTTC 161

QY       525 CTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATA 584
           |||||||||||||||||||||||||||||||||||||||
Db       162 CTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATA 221

QY       585 TGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGG 644
           |||||||||||||||||||||||||||||||||||||||
Db       222 TGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGG 281

QY       645 GGAGTATGTCTGCGAG 660
           |||||||||||||
Db       282 GGAGTATGTCTGCGAG 297

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RESULT 12

```

BI651936
LOCUS          BI651936              795 bp      mRNA      linear      EST 12-SEP-2001
DEFINITION    603298677F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5339251 5',
              mRNA sequence.
ACCESSION     BI651936
VERSION       BI651936.1  GI:15566172
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
              ORGANISM Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 795)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)

```


COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11861 row: j column: 20
 High quality sequence stop: 795.

FEATURES Location/Qualifiers
 source 1. .795
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129,C57BL/6J,FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5339251"
 /tissue_type="tumor, gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam3"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

ORIGIN

Query Match 23.4%; Score 210.2; DB 12; Length 795;
 Best Local Similarity 86.2%; Pred. No. 1.7e-32;
 Matches 244; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

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Qy      592 GGCAGAAAGAACTCACGAC-TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTA 650
          |||
Db      1   GGCAGAAAGAACTCACGGCTTACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTA 60

Qy      651 TGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAA 710
          |||
Db      61  CGTCTGTGAGGCCGAGAACATCCTTGGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAA 120

Qy      711 CAGCGTGAGCACCACCCTGTTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGC 770
          |||
Db      121 CAGCGTGAGCACCCTGTTCATCCTGGTCGGGACATGCCCGGAAGTGAATGAGACCGC 180

Qy      771 CAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTC 830
          |||
Db      181 CAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTC 240

Qy      831 CTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
          |||
Db      241 CTGCAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAG 283
  
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RESULT 13
 BE648780

LOCUS BE648780 259 bp mRNA linear EST 06-SEP-2000
 DEFINITION UI-M-BH2.2-aop-b-12-0-UI.r1 NIH_BMAP_M_S3.2 Mus musculus cDNA clone
 UI-M-BH2.2-aop-b-12-0-UI 5', mRNA sequence.
 ACCESSION BE648780
 VERSION BE648780.1 GI:9974601
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 259)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov
 cDNA Library Preparation: M.B. Soares Lab Clone distribution:
 Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
 should be noted that Bento Soares is generating a small number of
 additional specialized non-redundant arrays of BMAP cDNAs whose
 availability will be considered under appropriate and limited
 collaborative arrangements
 Seq primer: M13 Reverse.
 FEATURES
 source Location/Qualifiers
 1. .259
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH2.2-aop-b-12-0-UI"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_M_S3.2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_M_S3.2 library is a subtracted library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 brain (cerebellum, brain stems, olfactory bulbs,
 hypothalamus, cortex, amygdala, basal ganglia, pineal
 gland, striatum, hippocampus) after a series of
 subtractions to reduce the representation of cDNAs from
 which ESTs had already been generated. The following
 serially subtracted libraries were generated in this
 process: NIH_BMAP_M_S3.2, NIH_BMAP_M_S2, NIH_BMAP_M_S1.
 The subtracted library (NIH_BMAP_M_S3.2) was constructed
 as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S2
 clones from which 3' ESTs had been derived was used as a
 driver in a hybridization with the NIH_BMAP_M_S2 library

in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S3.2 library. This procedure has been previously described (Bonardo, Lennon and Soares, Genome Research 6:791-806, 1996)"

ORIGIN

```

Query Match          21.8%; Score 195.2; DB 10; Length 259;
Best Local Similarity 90.1%; Pred. No. 1.2e-29;
Matches 209; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      | | ||||| ||||| ||||| ||||| || || ||||| |||||
Db      1 CCACAACATCCTTGGGAAAGACACCGTGAGGGGCGACTCCATGTCAAGAGCGTGAGCAC 60

Qy      723 CACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
      ||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      61 CACTCTGTCATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTG 120

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 TGTGAATGGGGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 180

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCC 894
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 TGTGGGATACACCGGTGACAAGTGTGAGCAGTTCGCAATGGTCAACTTCTCC 232

```

RESULT 14

AA968077

```

LOCUS      AA968077          327 bp      mRNA      linear      EST 19-MAY-1998
DEFINITION uh09h01.r1 Soares mouse hypothalamus NMHy Mus musculus cDNA clone
IMAGE:1617457 5' similar to TR:035073 035073 NTAK ALPHA2-1P ;, mRNA
sequence.
ACCESSION  AA968077
VERSION    AA968077.1  GI:3141970
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 327)
AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE      The WashU-HHMI Mouse EST Project
JOURNAL    Unpublished (1996)
COMMENT    Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800

```

Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:956757
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 318.

FEATURES
 source Location/Qualifiers
 1. .327
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1617457"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse hypothalamus NMHy"
 /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGGCCCAAGGTTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Wolfgang Liedtke. Library went through
 two rounds of normalization, and was constructed by Bento
 Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 21.8%; Score 195.2; DB 9; Length 327;
 Best Local Similarity 90.2%; Pred. No. 1.4e-29;
 Matches 231; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

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Qy      641 CTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGC 700
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2   CCGGGGAGTACGTCTGTGAGGCCCAGAACATCCTTGGAAGGACACCGTGAGGGA-CGAC 60

Qy      701 TTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCA 760
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61   TCCATGTCAACAGCGTGAG-ACCACTCTGTTCATCCTGGTCGGGACATGCCCGGAAGTGCA 119

Qy      761 ACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCA 820
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      120 ATGAGACCGCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCA 179

Qy      821 ACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAA 880
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      180 ACCAGCTCTCCTGCAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAA 239

Qy      881 TGGTCAACTTCTCCTA 896
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      240 TGGTCAACATCTCCAA 255
  
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RESULT 15
 BX089049/c

LOCUS BX089049 362 bp mRNA linear EST 23-JAN-2003
 DEFINITION BX089049 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone

IMAGp998M133119 ; IMAGE:1240116, mRNA sequence.
 ACCESSION BX089049
 VERSION BX089049.1 GI:27825909
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 362)
 AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
 Radelof,U., Schneider,D. and Korn,B.
 TITLE Human UnigeneSet - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGp998M133119.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human UnigeneSet - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-
 bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTACACAGGAAACAGCTATGAC.
 FEATURES
 source Location/Qualifiers
 1. .362
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGp998M133119 ; IMAGE:1240116"
 /tissue_type="parathyroid tumor"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_parathyroid_tumor_NbHPA"
 /note="Organ: parathyroid gland; Vector: pT7T3D
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGGAGCGCCGCACCAATTTTTTTTTTTTTTTTTT
 TTTT-3'], double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,
 NIH."
 ORIGIN
 Query Match 20.4%; Score 182.6; DB 13; Length 362;
 Best Local Similarity 85.3%; Pred. No. 5.3e-27;

Matches 203; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy	656	GCGAGGCCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCG	715
Db	362	GCGAGGCCCGAGAACATCCTGGGGAAGGACACCGTCCGGGNCCGGCTTTACGTCAACAGCG	303
Qy	716	TGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGT	775
Db	302	TGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGT	243
Qy	776	CCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCA	835
Db	242	CCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCA	183
Qy	836	AGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC	893
Db	182	AGGCACATGGGCTGCACTGCTTAGAACTTGGTACCCAGAGCCACCACTTCCCCATCTC	125

Search completed: August 15, 2004, 09:42:30
Job time : 2850.01 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 02:48:13 ; Search time 3828.5 Seconds
(without alignments)
10155.083 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
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 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						
No.	Score	Match	Length	DB	ID		Description	
<hr/>								
	1	849	94.6	3020	9	AB005060	AB005060 Homo sapi	
	2	847.4	94.5	2613	9	AK124504	AK124504 Homo sapi	
	3	835.4	93.1	1884	6	AR098145	AR098145 Sequence	
	4	835.4	93.1	1884	6	AR116617	AR116617 Sequence	
	5	784	87.4	3441	6	AR072052	AR072052 Sequence	
	6	738.6	82.3	993	6	AR072053	AR072053 Sequence	
	7	737	82.2	2947	10	D89995	D89995 Rattus sp.	
	8	737	82.2	3076	6	E16456	E16456 Rat mRNA fo	
	9	737	82.2	3077	10	D89996	D89996 Rattus sp.	
	10	427.8	47.7	1476	6	AR098146	AR098146 Sequence	
	11	427.8	47.7	1476	6	AR116618	AR116618 Sequence	
	12	427.8	47.7	2268	6	AR098155	AR098155 Sequence	
	13	427.8	47.7	2268	6	AR116627	AR116627 Sequence	
	14	425	47.4	2188	10	AB001576	AB001576 Rattus sp	
	15	424.8	47.4	118504	9	AC094080	AC094080 Homo sapi	
c	16	424.8	47.4	152838	2	AC011589	AC011589 Homo sapi	
	17	424.8	47.4	170797	9	AC011379	AC011379 Homo sapi	
	18	424.8	47.4	210675	2	AC026272	AC026272 Homo sapi	
	19	424	47.3	1054	6	AX406616	AX406616 Sequence	
	20	424	47.3	1054	9	HS2NRG01	AF119151 Homo sapi	
	21	405.4	45.2	1607	6	AR098144	AR098144 Sequence	
	22	405.4	45.2	1607	6	AR116616	AR116616 Sequence	
	23	405.4	45.2	2467	6	AR098143	AR098143 Sequence	
	24	405.4	45.2	2467	6	AR116615	AR116615 Sequence	
	25	387.2	43.2	139074	2	AC131191	AC131191 Mus muscu	
	26	384	42.8	253462	2	AC096477	AC096477 Rattus no	
	27	216.2	24.1	1207	6	AR072054	AR072054 Sequence	
	28	173	19.3	419	6	AX406617	AX406617 Sequence	
	29	173	19.3	419	9	HS2NRG02	AF119152 Homo sapi	
	30	173	19.3	120236	9	AC008523	AC008523 Homo sapi	
c	31	173	19.3	189049	9	AC008667	AC008667 Homo sapi	
	32	142.6	15.9	85703	2	AC020830	AC020830 Mus muscu	
	33	142.6	15.9	190228	10	AC127350	AC127350 Mus muscu	

	34	139.4	15.5	226038	2	AC106592	AC106592 Rattus no
	35	139.4	15.5	273080	2	AC098540	AC098540 Rattus no
c	36	139.4	15.5	302176	2	AC096479	AC096479 Rattus no
	37	130.2	14.5	163	10	AY227026	AY227026 Mus muscu
	38	124.6	13.9	493	6	AX406618	AX406618 Sequence
	39	124.6	13.9	493	9	HS2NRG03	AF119153 Homo sapi
	40	124	13.8	350	6	AX406619	AX406619 Sequence
	41	124	13.8	350	9	HS2NRG04	AF119154 Homo sapi
c	42	109.6	12.2	85703	2	AC020830	AC020830 Mus muscu
c	43	108.4	12.1	205280	2	BX323592	BX323592 Danio rer
	44	108.4	12.1	207840	5	BX005008	BX005008 Zebrafish
	45	97	10.8	172	10	D89997	D89997 Rattus sp.

ALIGNMENTS

RESULT 1

AB005060

LOCUS AB005060 3020 bp mRNA linear PRI 14-NOV-1997

DEFINITION Homo sapiens mRNA for NTAK, complete cds.

ACCESSION AB005060

VERSION AB005060.1 GI:2626738

KEYWORDS NTAK.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Higashiyama,S., Horikawa,M., Yamada,K., Ichino,N., Nakano,N., Nakagawa,T., Miyagawa,J., Matsushita,N., Nagatsu,T., Taniguchi,N. and Ishiguro,H.

TITLE A novel brain-derived member of the epidermal growth factor family that interacts with ErbB3 and ErbB4

JOURNAL J. Biochem. 122 (3), 675-680 (1997)

MEDLINE 98006324

PUBMED 9348101

REFERENCE 2 (bases 1 to 3020)

AUTHORS Ishiguro,H.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-1997) Hiroshi Ishiguro, Fujita Health University, ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan (E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

FEATURES Location/Qualifiers

source 1..3020

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="SK-N-SH"

/cell_type="neuroblastoma"

CDS 226..2778

/codon_start=1

/product="NTAK"

/protein_id="BAA23417.1"

/db_xref="GI:2626739"

/translation="MRQVCCSALPPPPLEKGRCSSYSDSSSSSSERSSSSSSSSSSESG
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MLLEFVSLACYSPSLKSVQDQAYKAPVVVEGKVQGLVPAGGSSSNSTREPPASGRVAL
 VKVLDKWPLRSGGLQREQVISVGSVCVPLERNQRYIFFLEPTEQPLVFKTAFAPLDTNG
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 ERRRATAPPYHDSVDSLSDSPHSERYVSALTTPARLSPVDFHYSLATQVPTFEITSPN
 SAHAVSLPPAAPISYRLAEQQPLLRHPAPPGGPGPGPGPGPGADMQRSYDSYYYPAA
 GPGPRRGTCALGGSGLSLPASPFRIPEDEYETTQECAPPPPPRPRARGASRRTSAGP
 RRWRRSRLNGLAAQARAARDSLSLSGSGGGSASASDDDADDADGALAAESTPFLGL
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polyA_site

3020

/note="39 A nucleotides"

ORIGIN

Query Match 94.6%; Score 849; DB 9; Length 3020;
 Best Local Similarity 98.3%; Pred. No. 5.5e-152;
 Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	60
Db	502	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	561
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	562	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	621
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	622	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	681
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	682	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	741
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	742	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	801
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	802	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	861
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	862	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	921
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	922	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	981
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	982	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	1041

Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
 |||
 Db 1042 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 1101
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||
 Db 1102 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 1161
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 |||
 Db 1162 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 1221
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 1222 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 1281
 Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||
 Db 1282 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 1341
 Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 || ||| | ||| ||| |||
 Db 1342 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1374

RESULT 2

AK124504

LOCUS AK124504 2613 bp mRNA linear PRI 09-SEP-2003

DEFINITION Homo sapiens cDNA FLJ42513 fis, clone BRACE2046295, highly similar to NTAK PROTEIN.

ACCESSION AK124504

VERSION AK124504.1 GI:34530302

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2613)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES Location/Qualifiers
 source 1. .2613
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="BRACE2046295"
 /tissue_type="cerebellum"
 /clone_lib="BRACE2"
 /note="cloning vector: pME18SFL3"

ORIGIN

Query Match 94.5%; Score 847.4; DB 9; Length 2613;
Best Local Similarity 98.2%; Pred. No. 1.1e-151;
Matches 857; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
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Db     436 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTTGCTCGCCTGC 495

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 555

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 615

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     616 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 675

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 735

Qy     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 795

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 855

Qy     421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 915

Qy     481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     916 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 975

Qy     541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
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Db 976 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 1035

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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Db 1036 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 1095

Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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Db 1096 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 1155

Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCC GGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Db 1156 ACCACCCTGTCATCCTGGTCGGGGCACGCCC GGAAGTGCAACGAGACAGCCAAGTCCTAT 1215

Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||

Db 1216 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGT 1275

Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db 1276 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1308

RESULT 3

AR098145

LOCUS AR098145 1884 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 5 from patent US 6074841.

ACCESSION AR098145

VERSION AR098145.1 GI:12807402

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1884)

AUTHORS Gearing, D.P. and Busfield, S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6074841-A 5 13-JUN-2000;

FEATURES Location/Qualifiers

source 1. .1884

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 93.1%; Score 835.4; DB 6; Length 1884;

Best Local Similarity 98.1%; Pred. No. 2.2e-149;

Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
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Db 218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 277

Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 |||

Db 278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db 338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
 Qy 301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 518 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC'TGAC 420
 ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
 Db 578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAC'TGGC 636
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Db 637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 697 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 816
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
 Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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 Db 997 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
 Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

RESULT 4

AR116617

LOCUS AR116617 1884 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 5 from patent US 6133423.

ACCESSION AR116617

VERSION AR116617.1 GI:14096939

KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1884)
 AUTHORS Gearing,D.P. and Busfield,S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6133423-A 5 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1. .1884
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 93.1%; Score 835.4; DB 6; Length 1884;
 Best Local Similarity 98.1%; Pred. No. 2.2e-149;
 Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	60
Db	218	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	277
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	278	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	337
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600
Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	816

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 |||
 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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 Db 937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
 Qy 781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
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 Db 997 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGT 1056
 Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

RESULT 5

AR072052

LOCUS AR072052 3441 bp DNA linear PAT 18-FEB-2000

DEFINITION Sequence 1 from patent US 5912326.

ACCESSION AR072052

VERSION AR072052.1 GI:7222940

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 3441)

AUTHORS Chang,H.

TITLE Cerebellum-derived growth factors

JOURNAL Patent: US 5912326-A 1 15-JUN-1999;

FEATURES Location/Qualifiers

source 1. .3441

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 87.4%; Score 784; DB 6; Length 3441;

Best Local Similarity 92.2%; Pred. No. 1.4e-139;

Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 ATGAGGCGGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
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 Db 180 ATGAGGCGGACCCGGCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239
 Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 |||
 Db 240 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299
 Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||
 Db 300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 359

SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 993)
 AUTHORS Chang,H.
 TITLE Cerebellum-derived growth factors
 JOURNAL Patent: US 5912326-A 3 15-JUN-1999;
 FEATURES Location/Qualifiers
 source 1. .993
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 82.3%; Score 738.6; DB 6; Length 993;
 Best Local Similarity 90.4%; Pred. No. 6.8e-131;
 Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	60
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTTCAAG	540
Db	481	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	541	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG	600

Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	883	CAGTCGCTCAAGTGTGAGGCGGCGGCGGGGAACCCCCAGCCTCCTATCGATGGTTCAAG	942
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	943	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG	1002
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	1003	AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG	1062
Qy	661	GCCGAGAACATCCTTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	1063	GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC	1122
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTAT	780
Db	1123	ACCACTCTGTCTGTCCTGGTCGGGGCACGCCCAGGAGTGAATGAGACAGCCAAGTCCTAC	1182
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	1183	TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT	1242
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
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PC      A61K48/00,
PC      C07H21/04, (C12N5/10,C12R1:91), (C12P21/02,C12R1:91); CC
strandedness: Double;
CC      topology: Linear;
FH      Key                      Location/Qualifiers
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FT                                  /organism='Rattus sp.'
FT                                  /cell_line='PC12'
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FT                                  /product='NTAK protein'.

FEATURES
    source                      Location/Qualifiers
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ORIGIN

Query Match      82.2%;   Score 737;   DB 6;   Length 3076;
Best Local Similarity  90.3%;   Pred. No. 1.3e-130;
Matches 788;   Conservative  0;   Mismatches  85;   Indels  0;   Gaps  0;

Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      616 TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db      736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 795

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855

Qy      301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTTAAGACGGCCTTTGCC 360
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Db      856 CGCTACATCTTTTTCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 915

Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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Db      916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975

Qy      421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db      976 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1035

Qy      481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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SGPL"
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ORIGIN

Query Match 82.2%; Score 737; DB 10; Length 3077;
Best Local Similarity 90.3%; Pred. No. 1.3e-130;
Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60  
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Db      557 ATGAGGCGCGACCCGGCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 616  
  
Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120  
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Db      617 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 676  
  
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Db      677 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 736  
  
Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240  
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Db      737 CCCGCCTCGGGTCGGGTGGCGTTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 796  
  
Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300  
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Db      797 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 856  
  
Qy      301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360  
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Db      857 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 916  
  
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QY 363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
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QY 423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
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 Db 158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

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QY 543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
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 Db 278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

QY 603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
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 Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

QY 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
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 Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

QY 723 CACCCTGTCATCCTGGTTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 782
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QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
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QY 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 11

AR116618

LOCUS AR116618 1476 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6133423.

ACCESSION AR116618

VERSION AR116618.1 GI:14096940

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1476)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6133423-A 7 17-OCT-2000;

FEATURES Location/Qualifiers

source 1. .1476

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 47.7%; Score 427.8; DB 6; Length 1476;
 Best Local Similarity 89.8%; Pred. No. 1.3e-71;
 Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
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Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
          |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
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Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
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Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
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Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

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Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
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Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
  
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RESULT 12

AR098155

LOCUS AR098155 2268 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 31 from patent US 6074841.

ACCESSION AR098155

VERSION AR098155.1 GI:12807412

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2268)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6074841-A 31 13-JUN-2000;

FEATURES Location/Qualifiers

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ORIGIN

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Best Local Similarity 89.8%;  Pred. No. 1.2e-71;
Matches 459;  Conservative 0;  Mismatches 52;  Indels 0;  Gaps 0;

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Db      98 CCGCGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
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Db      158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
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Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
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Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
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Db      458 CACCCTGTCATCCTGGTTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
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Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

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RESULT 13

AR116627

LOCUS AR116627 2268 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 31 from patent US 6133423.

ACCESSION AR116627

VERSION AR116627.1 GI:14096949

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2268)

SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (sites)
 AUTHORS Higashiyama,S., Horikawa,M., Yamada,K., Ichino,N., Nakano,N.,
 Nakagawa,T., Miyagawa,J., Matsushita,N., Nagatsu,T., Taniguchi,N.
 and Ishiguro,H.
 TITLE A novel brain-derived member of the epidermal growth factor family
 that interacts with ErbB3 and ErbB4
 JOURNAL J. Biochem. 122 (3), 675-680 (1997)
 MEDLINE 98006324
 PUBMED 9348101
 REFERENCE 2 (bases 1 to 2188)
 AUTHORS Ishiguro,H.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-1997) Hiroshi Ishiguro, Fujita Health University,
 ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan
 (E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 47.4%; Score 425; DB 10; Length 2188;
 Best Local Similarity 87.0%; Pred. No. 4.2e-71;
 Matches 467; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 337 TTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAG 396
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 Db 4 TTTT TTTT TTAAGACAGCCTTTGCCCCGTCGACCCTAACGGCAAAAACATCAAGAAAGAG 63

REFERENCE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 118504)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 COMMENT On Mar 27, 2002 this sequence version replaced gi:19224838.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.7% of Sequence;
 Estimated Total Number of Errors is 0.5.

FEATURES Location/Qualifiers
 source 1. .118504
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Query Match 47.4%; Score 424.8; DB 9; Length 118504;
 Best Local Similarity 94.2%; Pred. No. 3.5e-71;
 Matches 452; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

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Db	81190	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	81249
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	849	94.6	994	6	AAS18019	Aas18019 Human cDN
3	835.4	93.1	1884	2	AAV17814	Aav17814 Homo sapi
4	784	87.4	3441	2	AAT87922	Aat87922 Rat cereb
5	738.6	82.3	1803	2	AAT87923	Aat87923 Rat cereb
6	737	82.2	3076	2	AAV43674	Aav43674 Receptor
7	723.4	80.6	1863	7	ABS56035	Abs56035 cDNA enco

8	427.8	47.7	2268	2	AAV17816	Aav17816	Homo sapi
9	426.8	47.6	1474	7	ABS56036	Abs56036	cDNA enco
10	426.8	47.6	2266	7	ABS56045	Abs56045	cDNA enco
11	426.2	47.5	1476	2	AAV17815	Aav17815	Homo sapi
12	424	47.3	1054	6	ABL40993	Abl40993	Human neu
13	405.4	45.2	1607	2	AAV17813	Aav17813	Mus muscu
14	402.2	44.8	2467	2	AAV17812	Aav17812	Mus muscu
15	393.4	43.9	1561	7	ABS56034	Abs56034	cDNA enco
16	393.4	43.9	2442	7	ABS56033	Abs56033	cDNA enco
17	256	28.5	667	2	AAT87924	Aat87924	Human cer
18	173	19.3	419	6	ABL40994	Abl40994	Human neu
19	124.6	13.9	480	6	ABL40995	Abl40995	Human neu
20	124	13.8	350	6	ABL40996	Abl40996	Human neu
21	85.6	9.5	1986	2	AAZ32061	Aaz32061	Human MET
22	84	9.4	1986	5	AAC90318	Aac90318	L12260 cD
23	84	9.4	2003	2	AAT30995	Aat30995	Glial gro
24	84	9.4	2003	2	AAT48090	Aat48090	Human neu
25	84	9.4	2003	2	AAT06739	Aat06739	Glial gro
26	84	9.4	2003	2	AAZ32062	Aaz32062	Human MET
27	84	9.4	2003	5	AAC90319	Aac90319	I36352 cD
28	83.4	9.3	1108	2	AAQ30671	Aaq30671	GGF2BPP3.
29	83.4	9.3	1108	2	AAQ62850	Aaq62850	GGF-II cD
30	83.4	9.3	1108	2	AAQ58304	Aaq58304	GGF-II cD
31	83.4	9.3	1108	2	AAQ74886	Aaq74886	Putative
32	83.4	9.3	1108	2	AAT30998	Aat30998	Bovine gl
33	83.4	9.3	1108	2	AAT48080	Aat48080	Bovine ne
34	83.4	9.3	1108	2	AAT06704	Aat06704	Bovine gl
35	82.4	9.2	2003	2	AAQ62838	Aaq62838	GGF2HBS5.
36	82.4	9.2	2003	2	AAQ58329	Aaq58329	GGF2HBS5.
37	78.2	8.7	1027	5	AAF80062	Aaf80062	Nucleotid
38	78.2	8.7	3086	5	AAF80059	Aaf80059	Nucleotid
39	76.8	8.6	1140	2	AAQ62840	Aaq62840	GGF2BPP2.
40	76.8	8.6	1140	2	AAQ58321	Aaq58321	GGF2BPP2.
41	76.8	8.6	1140	2	AAQ74912	Aaq74912	Bovine gl
42	76.8	8.6	1140	2	AAT31001	Aat31001	Glial gro
43	76.8	8.6	1140	2	AAT48088	Aat48088	Human neu
44	76.8	8.6	1140	2	AAT06731	Aat06731	BPP2 glia
45	76.8	8.6	1140	2	AAX81201	Aax81201	Nucleotid

ALIGNMENTS

RESULT 1

AAS18020

ID AAS18020 standard; cDNA; 897 BP.

XX

AC AAS18020;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2beta, NRG-2beta.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;

KW cell survival; cell growth; cell differentiation; erbB receptor;

KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;

KW atherosclerosis; vascular lesion; vascular hypertension;

KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .897
 FT /*tag= a
 FT /product= "NRG-2beta"
 XX
 PN WO200189568-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016896.
 XX
 PR 23-MAY-2000; 2000US-0206495P.
 XX
 PA (CENE-) CENES PHARM INC.
 XX
 PI Marchionni MA;
 XX
 DR WPI; 2002-097612/13.
 DR P-PSDB; AAU11636.
 XX
 PT Neuregulin-2 polypeptide and polynucleotide useful for treating multiple
 PT sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's disease, by
 PT increasing mitogenesis, survival, growth or differentiation of a cell.
 XX
 PS Claim 57; Fig 8; 79pp; English.
 XX
 CC The invention relates to a substantially pure neuregulin (NRG)-2
 CC polypeptide comprising or consisting of a sequence for human NRG-2alpha
 CC or NRG-2beta (clone 2b7) and the polynucleotides encoding the. Also
 CC included are a vector expressing the protein, a host cell comprising the
 CC vector, a transgenic non-human animal transformed with the vector or
 CC having a knockout mutation in one or both NRG-2 alleles and an anti-NRG-2
 CC antibody. Analysis of mutations in NRG-2 in an individual is useful for
 CC diagnosing an increased likelihood of developing a NRG-2-related disease
 CC or condition in a test subject. NRG-2 is useful for increasing the
 CC mitogenesis, survival, growth or differentiation of a cell (e.g. a
 CC neuronal cell), where the cell expresses an erbB receptor. NRG-2 is
 CC useful for treating diseases and disorders such as cardiomyopathy
 CC (preferably degenerative congenital disease), ischaemic damage, cardiac
 CC trauma or heart failure or which has a condition affecting smooth muscle
 CC which include atherosclerosis, vascular lesion, vascular hypertension,
 CC and degenerative congenital vascular disease, myasthenia gravis, a
 CC neurodegenerative disorder, peripheral neuropathy, a sensory nerve fiber
 CC neuropathy, a motor fiber and a sensory nerve fiber neuropathy, multiple
 CC sclerosis, amyotrophic lateral sclerosis, spinal muscular atrophy, nerve
 CC injury, Alzheimer's disease, Parkinson's disease, cerebellar ataxia, and
 CC spinal cord injury. The antibody is useful for treatment of a tumour

CC comprising inhibiting proliferation of a tumour cell preferably a glial
CC tumour cell, for treating of neurofibromatosis by inhibiting glial cell
CC mitogenesis. The present sequence encodes NRG-2beta

XX

SQ Sequence 897 BP; 200 A; 261 C; 282 G; 154 T; 0 U; 0 Other;

Query Match 100.0%; Score 897; DB 6; Length 897;

Best Local Similarity 100.0%; Pred. No. 1.5e-195;

Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60

Qy     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

Qy    121 GGCAAGGTACAGGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGCAAGGTACAGGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180

Qy    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300

Qy    301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

Qy    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480

Qy    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540

Qy    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600

Qy    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660

Qy    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
```

Qy 721 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCAGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 721 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCAGGAAGTGCAACGAGACAGCCAAGTCCTAT 780

Qy 781 TCGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||
 Db 781 TCGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840

Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA 897
 |||
 Db 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA 897

RESULT 2

AAS18019

ID AAS18019 standard; cDNA; 994 BP.

XX

AC AAS18019;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2alpha, NRG-2alpha.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;
 KW cell survival; cell growth; cell differentiation; erbB receptor;
 KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;
 KW atherosclerosis; vascular lesion; vascular hypertension;
 KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1. .993
FT		/*tag= a
FT		/product= "NRG-2alpha"

XX

PN WO200189568-A1.

XX

PD 29-NOV-2001.

XX

PF 23-MAY-2001; 2001WO-US016896.

XX

PR 23-MAY-2000; 2000US-0206495P.

XX

PA (CENE-) CENES PHARM INC.

XX

PI Marchionni MA;

XX

DR WPI; 2002-097612/13.

DR P-PSDB; AAU11635.

Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCAGGAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCAGGAGTGCAACGAGACAGCCAAGTCCTAT	780
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	841	CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	873

RESULT 3

AAV17814

ID AAV17814 standard; cDNA; 1884 BP.

XX

AC AAV17814;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;

KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;

KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;

KW wound healing; transmembrane; ss.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 664..1884
 FT /*tag= a
 FT /note= "don-1 polypeptide"
 XX
 PN WO9807736-A1.
 XX
 PD 26-FEB-1998.
 XX
 PF 18-AUG-1997; 97WO-US014585.
 XX
 PR 19-AUG-1996; 96US-00699591.
 PR 19-NOV-1996; 96US-00753007.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 1998-169084/15.
 DR P-PSDB; AAW48381.
 XX
 PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.
 XX
 PS Claim 4; Fig 3; 121pp; English.
 XX
 CC The sequence is that of a human don-1 gene splice variant. Don-1
 CC polypeptides stimulate proliferation of epithelial cells and thus are
 CC implicated in melanomas and adenocarcinomas in which epithelial cells
 CC proliferate out of control. Compounds that interfere with don-1 mediated
 CC cell proliferation can be used in the treatment of tumours such as
 CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
 CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
 CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
 CC cell proliferation, e.g. for wound healing
 XX
 SQ Sequence 1884 BP; 426 A; 607 C; 560 G; 291 T; 0 U; 0 Other;

Query Match 93.1%; Score 835.4; DB 2; Length 1884;
 Best Local Similarity 98.1%; Pred. No. 2.2e-181;
 Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277
 Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337
 Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Db	398		CCCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241		GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458		GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301		CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518		CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361		CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578		CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421		TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637		TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481		CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697		CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541		GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	757		GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG	816
Qy	601		AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817		AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661		GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877		GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721		ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937		ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781		TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	997		TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGT	1056
Qy	841		CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	1057		CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	1089

RESULT 4

AAT87922

ID AAT87922 standard; cDNA; 3441 BP.

XX

AC AAT87922;

XX

DT 18-DEC-1997 (first entry)

XX

DE Rat cerebellum derived growth factor 1 cDNA.

XX
 KW Rat; cerebellum derived growth factor; CDGF1; screening; binding;
 KW modulation; erbB type receptor; identification; indication; risk;
 KW proliferation; differentiation; induction; neuron; hyperplasia;
 KW stem cell culture; intracerebral graft; alleviation; repair;
 KW behavioural defect; nervous system; central; peripheral; nerve;
 KW prosthesis; damage; entubulation; cell survival; treatment; injury;
 KW trauma; ischaemia; ischemia; stroke; infection; disorder; inflammation;
 KW neurodegeneration; disease; Parkinson's; Huntingdon's;
 KW amyotrophic lateral sclerosis; sensory; retina;
 KW spinocerebellar degeneration; multiple sclerosis; neoplasia;
 KW amalignant glioma; medulloblastoma; neuroectodermal tumour; ds.
 XX
 OS Rattus rattus.
 XX
 FH Key Location/Qualifiers
 FT CDS 180. .2444
 FT /*tag= a
 FT sig_peptide 180. .248
 FT /*tag= b
 FT mat_peptide 249. .2441
 FT /*tag= c
 FT /product= "cerebellum_derived_growth_factor"
 XX
 PN WO9709425-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 09-SEP-1996; 96WO-US014484.
 XX
 PR 08-SEP-1995; 95US-00525864.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (STRD) UNIV LELAND S STANFORD.
 XX
 PI Chang H;
 XX
 DR WPI; 1997-192900/17.
 DR P-PSDB; AAW27536.
 XX
 PT Rat and human cerebellum-derived growth factors - used in the treatment
 PT of neuronal injury and proliferative disorders.
 XX
 PS Claim 17; Page 63-66; 94pp; English.
 XX
 CC The present sequence encodes rat cerebellum derived growth factor 1
 CC (CDGF1), which can be used to screen for modulators of CDGF binding to
 CC erbB type receptors. Identification of a modification or mutation in a
 CC CDGF gene, or aberrant expression of a CDGF gene or levels of soluble
 CC CDGF may be used to indicate the risk of unwanted cell proliferation or
 CC differentiation. CDGF may be used to induce neuronal differentiation in
 CC stem cell culture, and maintain the integrity of a terminally
 CC differentiated neuronal cell culture, e.g. useful for intracerebral
 CC grafting to alleviate behavioural defects. CDGF may also be used in nerve
 CC prostheses to repair central and peripheral nerve damage, especially where
 CC a crushed or severed axon is entubulated by a prosthetic. CDGF may also
 CC be used to enhance neuronal cell survival in the central or peripheral

nervous system, to treat neurological conditions associated with nervous system injury, e.g. traumatic, chemical or vasal injury and deficits such as ischaemia resulting from stroke, infectious/inflammatory and tumour induced injury, chronic neurodegenerative disease including Parkinson's and Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar degeneration, chronic immunological disease of the nervous system including multiple sclerosis, disorders of the sensory neurons and degenerative diseases of the retina. CDGF may also be used to treat neoplastic or hyperplastic transformations, particularly of the central nervous system, e.g. amalignant gliomas, medulloblastomas and neuroectodermal tumours

Sequence 3441 BP; 777 A; 1057 C; 1015 G; 592 T; 0 U; 0 Other;

Query Match 87.4%; Score 784; DB 2; Length 3441;

Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTGCTCGCCTGC	60
Db	180	ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	239
Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	240	TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	299
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	300	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	359
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	360	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	419
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	420	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	479
Qy	301	CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	480	CGCTACATCTTTTTCTGGAGCCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	539
Qy	361	CCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	540	CCGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	599
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	600	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	659
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	660	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG	719
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600
Db	720	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTGCGATCAAGTATGGCAACGGCAGAAAG	779

PD 13-MAR-1997.
 XX
 PF 09-SEP-1996; 96WO-US014484.
 XX
 PR 08-SEP-1995; 95US-00525864.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (STRD) UNIV LELAND S STANFORD.
 XX
 PI Chang H;
 XX
 DR WPI; 1997-192900/17.
 DR P-PSDB; AAW27537.
 XX
 PT Rat and human cerebellum-derived growth factors - used in the treatment
 PT of neuronal injury and proliferative disorders.
 XX
 PS Claim 17; Page 70-74; 94pp; English.
 XX
 CC The present sequence encodes rat cerebellum derived growth factor 2
 CC (CDGF2), which can be used to screen for modulators of CDGF binding to
 CC erbB type receptors. Identification of a modification or mutation in a
 CC CDGF gene, or aberrant expression of a CDGF gene or levels of soluble
 CC CDGF may be used to indicate the risk of unwanted cell proliferation or
 CC differentiation. CDGF may be used to induce neuronal differentiation in
 CC stem cell culture, and maintain the integrity of a terminally
 CC differentiated neuronal cell culture, e.g. useful for intracerebral
 CC grafting to alleviate behavioural defects. CDGF may also be used in nerve
 CC prostheses to repair central and peripheral nerve damage, especially where
 CC a crushed or severed axon is entubulated by a prosthetic. CDGF may also
 CC be used to enhance neuronal cell survival in the central or peripheral
 CC nervous system, to treat neurological conditions associated with nervous
 CC system injury, e.g. traumatic, chemical or vasal injury and deficits such
 CC as ischaemia resulting from stroke, infectious/inflammatory and tumour
 CC induced injury, chronic neurodegenerative disease including Parkinson's
 CC and Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar
 CC degeneration, chronic immunological disease of the nervous system
 CC including multiple sclerosis, disorders of the sensory neurons and
 CC degenerative diseases of the retina. CDGF may also be used to treat
 CC neoplastic or hyperplastic transformations, particularly of the central
 CC nervous system, e.g. amalignant gliomas, medulloblastomas and
 CC neuroectodermal tumours
 XX
 SQ Sequence 1803 BP; 408 A; 549 C; 537 G; 309 T; 0 U; 0 Other;

Query Match 82.3%; Score 738.6; DB 2; Length 1803;
 Best Local Similarity 90.4%; Pred. No. 3e-159;
 Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	60
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120

Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCAGCCCTCCTATCGATGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	541	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG	600
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	601	AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG	660
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	661	GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACTCTGTCTGTCCTGGTCGGGGCACGCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC	780
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	781	TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT	840
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	841	CCAAACGGATTCTTCGGACAGAGATGTTTGGAG	873

RESULT 6

AAV43674

ID AAV43674 standard; cDNA; 3076 BP.

XX

AC AAV43674;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Receptor type tyrosine kinase ErbB ligand encoding cDNA.
 XX
 KW Receptor type tyrosine kinase ErbB; ligand; diagnostic agent;
 KW nervous disease; cancer; ss.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 232..2814
 FT /*tag= a
 FT /product= "ligand of receptor type tyrosine kinase ErbB"
 XX
 PN JP10179166-A.
 XX
 PD 07-JUL-1998.
 XX
 PF 25-DEC-1996; 96JP-00356998.
 XX
 PR 25-DEC-1996; 96JP-00356998.
 XX
 PA (HIGA/) HIGASHIYAMA S.
 XX
 DR WPI; 1998-430952/37.
 DR P-PSDB; AAW63700.
 XX
 PT Gene coding the ligand of the tyrosine kinase ErbB receptor - useful for
 PT diagnosing and treating nervous diseases and cancer.
 XX
 PS Example; Page 9-13; 17pp; Japanese.
 XX
 CC This cDNA encodes the ligand of receptor type tyrosine kinase ErbB. A
 CC prokaryotic or eukaryotic host cell transformed by a recombinant vector
 CC containing the encoding DNA can be used for the recombinant production of
 CC the protein. The invention provides a method for inhibiting the formation
 CC of the ligand of receptor type tyrosine kinase ErbB in an animal using an
 CC antibody recognizing the protein. The ligand of the tyrosine kinase ErbB
 CC receptor and associated materials can be used for treating or diagnosing
 CC nervous diseases and cancers
 XX
 SQ Sequence 3076 BP; 673 A; 996 C; 944 G; 463 T; 0 U; 0 Other;

Query Match 82.2%; Score 737; DB 2; Length 3076;
 Best Local Similarity 90.3%; Pred. No. 7.9e-159;
 Matches 788; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
 ||||||||||||||||||||||||| ||| ||||||||||||||||||| ||||||||
 Db 556 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 615
 Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 ||||||||||||||||||||| |||||||||||||||||||||||||||||
 Db 616 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675

Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||||
 Db 676 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 735

Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||||
 Db 736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 795

Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 |||||
 Db 796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855

Qy 301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||||
 Db 856 CGCTACATCTTTTTCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 915

Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 || |||||
 Db 916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975

Qy 421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 |||||
 Db 976 TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1035

Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 || |||||
 Db 1036 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 1095

Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
 || |||||
 Db 1096 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG 1155

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||||
 Db 1156 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 1215

Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 || |||||
 Db 1216 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 1275

Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||||
 Db 1276 ACCACTCTGTCTCCTGGTCGGGGCACGCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 1335

Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 || || |||||
 Db 1336 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1395

Qy 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 || |||||
 Db 1396 CCAAACGGATTCTTCGGACAGAGATGTTTGGAG 1428

RESULT 7

ABS56035

ID ABS56035 standard; cDNA; 1863 BP.

XX

AC ABS56035;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE cDNA encoding human membrane-bound splice variant of Don-1.
 XX
 KW Human; Don-1; epidermal growth factor; EGF; neuregulin;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 643..1863
 FT /*tag= a
 FT /partial
 FT /product= "Membrane-bound splice variant of Don-1"
 FT /note= "This sequence lacks a stop codon"
 XX
 PN US2002127594-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 12-MAR-2002; 2002US-00096241.
 XX
 PR 22-JUN-2000; 2000US-00599789.
 XX
 PA (GEAR/) GEARING D P.
 PA (BUSF/) BUSFIELD S J.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 2003-039584/03.
 DR P-PSDB; ABG71638.
 XX
 PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
 PT for identifying proteins that interact with Don-1, and for regulating
 PT tumor formation and progression in brain.
 XX
 PS Claim 4; Fig 3; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel gene called Don
 CC -1, and alternate splice variants of Don-1, which are related to
 CC epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides
 CC are glycoprotein ligands. Both murine and human Don-1 sequences are
 CC cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides
 CC are useful for stimulating proliferation of a cell. Antibodies to Don-1
 CC polypeptides are useful for detecting Don-1 in a sample. The Don-1
 CC polypeptides are useful for treating and diagnosing cell proliferative
 CC disorders and play a role in the proliferation of carcinomas e.g.
 CC adenocarcinoma, myeloma, in cell differentiation, proliferation and
 CC survival. The polypeptides are also useful for inhibiting proliferation
 CC of adenocarcinoma cells, for stimulating the proliferation of cells such
 CC as epithelial cells to promote wound healing, for identifying proteins
 CC that interact with Don-1, and for regulating tumour formation and

CC progression in the brain. The polynucleotide sequences encoding Don-1 may
CC be used in gene therapy. The present sequence encodes human membrane-
CC bound splice variant of Don-1

XX

SQ Sequence 1863 BP; 422 A; 602 C; 553 G; 286 T; 0 U; 0 Other;

Query Match 80.6%; Score 723.4; DB 7; Length 1863;
Best Local Similarity 96.2%; Pred. No. 9.2e-156;
Matches 840; Conservative 0; Mismatches 16; Indels 17; Gaps 9;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
          |||
Db     213 ATGAGGCGCGACCCGGCCCCC--CTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 270

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          |||
Db     271 TACTCGCCAGCCTCAAGTCA--GCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 328

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
          |||
Db     329 GGCAAGGTACAGGGGCTGGT--CAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 386

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
          |||
Db     387 CCCGCCTCGGGTCGGGTGGCG--GGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 444

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db     445 GGGCTGCAGCGCGAGCAGGTG--CAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 502

Qy     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db     503 CGCTACATCTTTTTCCTGGAG--CACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 560

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          |||
Db     561 CCCCT-GATACCAACGGCAAAA--CTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 617

Qy     421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
          |||
Db     618 TGCGCCACCCGGCCCCAAGTTGA--AAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 675

Qy     481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
          |||
Db     676 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 735

Qy     541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
          |||
Db     736 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 795

Qy     601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
          |||
Db     796 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 855

Qy     661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
          |||
Db     856 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 915
```

QY 721 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 916 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 975
 QY 781 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 |||
 Db 976 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAAATGT 1035
 QY 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 || ||| | || | || || ||
 Db 1036 CCAAAATGGATTCTTCGGACAGAGATGTTTGGAG 1068

RESULT 8

AAV17816

ID AAV17816 standard; cDNA; 2268 BP.

XX

AC AAV17816;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;
 KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
 KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
 KW wound healing; transmembrane; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 69. .2012

FT /*tag= a

FT /note= "don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US014585.

XX

PR 19-AUG-1996; 96US-00699591.

PR 19-NOV-1996; 96US-00753007.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48383.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.

XX

PS Claim 4; Fig 7; 121pp; English.

XX

CC The sequence is that of a human don-1 gene splice variant. Don-1
CC polypeptides stimulate proliferation of epithelial cells and thus are
CC implicated in melanomas and adenocarcinomas in which epithelial cells
CC proliferate out of control. Compounds that interfere with don-1 mediated
CC cell proliferation can be used in the treatment of tumours such as
CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
CC cell proliferation, e.g. for wound healing

XX

SQ Sequence 2268 BP; 502 A; 735 C; 700 G; 331 T; 0 U; 0 Other;

Query Match 47.7%; Score 427.8; DB 2; Length 2268;
Best Local Similarity 89.8%; Pred. No. 4.1e-88;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

```
Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | | | | | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 782
      |||||
Db      458 CACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
      |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
      |||| | || | || | ||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608
```

RESULT 9

ABS56036

ID ABS56036 standard; cDNA; 1474 BP.

XX

AC ABS56036;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE cDNA encoding human second splice variant of Don-1.
 XX
 KW Human; Don-1; epidermal growth factor; EGF; neuregulin;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 68. .1473
 FT /*tag= a
 FT /partial
 FT /product= "Second splice variant of Don-1"
 FT /note= "This sequence lacks a stop codon"
 FT /transl_except= (pos:107. .108, aa:Lys)
 FT /note= "This codon has an apparent 1 nucleotide deletion
 FT which alters the reading frame"
 XX
 PN US2002127594-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 12-MAR-2002; 2002US-00096241.
 XX
 PR 22-JUN-2000; 2000US-00599789.
 XX
 PA (GEAR/) GEARING D P.
 PA (BUSF/) BUSFIELD S J.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 2003-039584/03.
 DR P-PSDB; ABG71639.
 XX
 PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
 PT for identifying proteins that interact with Don-1, and for regulating
 PT tumor formation and progression in brain.
 XX
 PS Claim 4; Fig 4; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel gene called Don
 CC -1, and alternate splice variants of Don-1, which are related to
 CC epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides
 CC are glycoprotein ligands. Both murine and human Don-1 sequences are
 CC cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides
 CC are useful for stimulating proliferation of a cell. Antibodies to Don-1
 CC polypeptides are useful for detecting Don-1 in a sample. The Don-1
 CC polypeptides are useful for treating and diagnosing cell proliferative
 CC disorders and play a role in the proliferation of carcinomas e.g.
 CC adenocarcinoma, myeloma, in cell differentiation, proliferation and
 CC survival. The polypeptides are also useful for inhibiting proliferation

XX
 DE cDNA encoding human third splice variant of Don-1.
 XX
 KW Human; Don-1; epidermal growth factor; EGF; neuregulin;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 68..2010
 FT /*tag= a
 FT /product= "Third splice variant of Don-1"
 FT /transl_except= (pos:107..108, aa:Lys)
 FT /note= "This codon has an apparent 1 nucleotide deletion
 FT which alters the reading frame"
 FT /transl_except= (pos:994..996, aa:Thr)
 XX
 PN US2002127594-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 12-MAR-2002; 2002US-00096241.
 XX
 PR 22-JUN-2000; 2000US-00599789.
 XX
 PA (GEAR/) GEARING D P.
 PA (BUSF/) BUSFIELD S J.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 2003-039584/03.
 DR P-PSDB; ABG71644.
 XX
 PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
 PT for identifying proteins that interact with Don-1, and for regulating
 PT tumor formation and progression in brain.
 XX
 PS Claim 4; Fig 7; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel gene called Don
 CC -1, and alternate splice variants of Don-1, which are related to
 CC epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides
 CC are glycoprotein ligands. Both murine and human Don-1 sequences are
 CC cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides
 CC are useful for stimulating proliferation of a cell. Antibodies to Don-1
 CC polypeptides are useful for detecting Don-1 in a sample. The Don-1
 CC polypeptides are useful for treating and diagnosing cell proliferative
 CC disorders and play a role in the proliferation of carcinomas e.g.
 CC adenocarcinoma, myeloma, in cell differentiation, proliferation and
 CC survival. The polypeptides are also useful for inhibiting proliferation
 CC of adenocarcinoma cells, for stimulating the proliferation of cells such
 CC as epithelial cells to promote wound healing, for identifying proteins
 CC that interact with Don-1, and for regulating tumour formation and
 CC progression in the brain. The polynucleotide sequences encoding Don-1 may

KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
KW wound healing; transmembrane; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 69. .1475

FT /*tag= a

FT /note= "don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US014585.

XX

PR 19-AUG-1996; 96US-00699591.

PR 19-NOV-1996; 96US-00753007.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48382.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
PT and adenocarcinoma(s), and for wound healing.

XX

PS Claim 4; Fig 4; 121pp; English.

XX

CC The sequence is that of a human don-1 gene splice variant. Don-1
CC polypeptides stimulate proliferation of epithelial cells and thus are
CC implicated in melanomas and adenocarcinomas in which epithelial cells
CC proliferate out of control. Compounds that interfere with don-1 mediated
CC cell proliferation can be used in the treatment of tumours such as
CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
CC cell proliferation, e.g. for wound healing

XX

SQ Sequence 1476 BP; 335 A; 475 C; 450 G; 216 T; 0 U; 0 Other;

Query Match 47.5%; Score 426.2; DB 2; Length 1476;

Best Local Similarity 89.6%; Pred. No. 8.6e-88;

Matches 458; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422

|| || | || | | | | || | || | || | ||

Db 98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy 423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482

|||||

Db 158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy 483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542

Db	218		ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543		TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278		TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603		CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338		CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663		CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398		CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723		CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db	458		CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG	517
Qy	783		CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC	842
Db	518		CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC	577
Qy	843		TGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	578		AAATGGATTCTTCGCACAGAGATGTTTGGAG	608

RESULT 12

ABL40993

ID ABL40993 standard; DNA; 1054 BP.

XX

AC ABL40993;

XX

DT 03-JUL-2002 (first entry)

XX

DE Human neuregulin 2 gene exon 1.

XX

KW Human; MUC1; mucin; glycoprotein; cytostatic; cancer; tumour; ECD;

KW extracellular domain; neuregulin 2; isoform; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200222685-A2.

XX

PD 21-MAR-2002.

XX

PF 11-SEP-2001; 2001WO-US028548.

XX

PR 11-SEP-2000; 2000US-0231841P.

XX

PA (KUFE/) KUFE D W.

PA (OHNO/) OHNO T.

XX

PI Kufe DW, Ohno T;

XX

DR WPI; 2002-339864/37.

XX
PT Use of a mucin glycoprotein (MUC1) extracellular domain antagonist for
PT manufacturing a medicant that inhibits the proliferation of MUC-1
PT expressing cancer cells and that can treat cancers and reduce tumor
PT growth.
XX
PS Disclosure; Page 61-62; 74pp; English.
XX
CC The invention relates to the use of a MUC1 (mucin glycoprotein)
CC extracellular domain (ECD) antagonist for the manufacture of a medicant
CC to inhibit the proliferation of MUC-1 expressing cancer cells. MUC1 ECD
CC antagonists (optionally combined with a pharmaceutical carrier) can be
CC administered to inhibit proliferation of MUC1-expressing cancer cells,
CC useful to treat cancers e.g. skin cancer, prostate cancer and leukemia,
CC especially in humans. The method may also be combined with administration
CC of a chemotherapeutic agent (e.g. an alkylating agent, topoisomerase etc)
CC or radiation to treat cancer, especially to reduce tumour growth. The
CC polypeptides are also useful in screening to identify MUC1 ECD
CC antagonists. The present sequence represents an exon fragment of the
CC human neuregulin 2 gene
XX
SQ Sequence 1054 BP; 178 A; 367 C; 361 G; 148 T; 0 U; 0 Other;

Query Match 47.3%; Score 424; DB 6; Length 1054;
Best Local Similarity 100.0%; Pred. No. 2.5e-87;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	589	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	648
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	649	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	708
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	709	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	768
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	769	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	828
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG	300
Db	829	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG	888
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	889	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	948
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	949	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	1008
Qy	421	TGCG	424

Db 1009 TGCG 1012

RESULT 13

AAV17813

ID AAV17813 standard; cDNA; 1607 BP.

XX

AC AAV17813;

XX

DT 17-AUG-1998 (first entry)

XX

DE Mus musculus don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;

KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;

KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;

KW wound healing; secreted protein; ss.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT CDS 79. .624

FT /*tag= a

FT /note= "secreted don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US014585.

XX

PR 19-AUG-1996; 96US-00699591.

PR 19-NOV-1996; 96US-00753007.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48380.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas and adenocarcinoma(s), and for wound healing.

XX

PS Claim 4; Fig 2; 121pp; English.

XX

CC The sequence is that of a murine don-1 gene splice variant. Don-1
CC polypeptides stimulate proliferation of epithelial cells and thus are
CC implicated in melanomas and adenocarcinomas in which epithelial cells
CC proliferate out of control. Compounds that interfere with don-1 mediated
CC cell proliferation can be used in the treatment of tumours such as
CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
CC cell proliferation, e.g. for wound healing

XX

SQ Sequence 1607 BP; 365 A; 500 C; 480 G; 262 T; 0 U; 0 Other;


```

OS      Mus musculus.
XX
FH      Key                Location/Qualifiers
FT      CDS                79..1896
FT                        /*tag= a
FT                        /note= "transmembrane don-1 polypeptide"
XX
PN      WO9807736-A1.
XX
PD      26-FEB-1998.
XX
PF      18-AUG-1997;      97WO-US014585.
XX
PR      19-AUG-1996;      96US-00699591.
PR      19-NOV-1996;      96US-00753007.
XX
PA      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI      Gearing DP,      Busfield SJ;
XX
DR      WPI; 1998-169084/15.
DR      P-PSDB; AAW48379.
XX
PT      Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
PT      and adenocarcinoma(s), and for wound healing.
XX
PS      Claim 4; Fig 1; 121pp; English.
XX
CC      The sequence is that of a murine don-1 gene splice variant. Don-1
CC      polypeptides stimulate proliferation of epithelial cells and thus are
CC      implicated in melanomas and adenocarcinomas in which epithelial cells
CC      proliferate out of control. Compounds that interfere with don-1 mediated
CC      cell proliferation can be used in the treatment of tumours such as
CC      melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
CC      liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
CC      Alternatively, don-1 polypeptides can be used to stimulate epithelial
CC      cell proliferation, e.g. for wound healing
XX
SQ      Sequence 2467 BP; 592 A; 752 C; 706 G; 417 T; 0 U; 0 Other;

Query Match                44.8%;  Score 402.2;  DB 2;  Length 2467;
Best Local Similarity      87.5%;  Pred. No. 3e-82;
Matches 440;  Conservative 0;  Mismatches 63;  Indels 0;  Gaps 0;

QY      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
      | |||||
DB      2 CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

QY      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
      |||||
DB      62 GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

QY      491 AGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCTACCGTTGGTTCAAGGATGGCAAGG 550
      |||||
DB      122 AGTGTGAGGCAGCGCGGGAAACCCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181

QY      551 AGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610

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PA (BUSF/) BUSFIELD S J.

XX
PI Gearing DP, Busfield SJ;
XX
DR WPI; 2003-039584/03.
DR P-PSDB; ABG71637.

PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
PT for identifying proteins that interact with Don-1, and for regulating
PT tumor formation and progression in brain.

PS Claim 4; Fig 2; 66pp; English.

The present invention relates to the isolation of a novel gene called Don-1, and alternate splice variants of Don-1, which are related to epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides are glycoprotein ligands. Both murine and human Don-1 sequences are cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides are useful for stimulating proliferation of a cell. Antibodies to Don-1 polypeptides are useful for detecting Don-1 in a sample. The Don-1 polypeptides are useful for treating and diagnosing cell proliferative disorders and play a role in the proliferation of carcinomas e.g. adenocarcinoma, myeloma, in cell differentiation, proliferation and survival. The polypeptides are also useful for inhibiting proliferation of adenocarcinoma cells, for stimulating the proliferation of cells such as epithelial cells to promote wound healing, for identifying proteins that interact with Don-1, and for regulating tumour formation and progression in the brain. The polynucleotide sequences encoding Don-1 may be used in gene therapy. The present sequence encodes murine secreted splice variant of Don-1

SQ Sequence 1561 BP; 361 A; 479 C; 465 G; 256 T; 0 U; 0 Other;

Query Match 43.9%; Score 393.4; DB 7; Length 1561;
Best Local Similarity 87.7%; Pred. No. 2.8e-80;
Matches 441; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY	371	CCAACGGCAAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACC	430
Db	2	CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCA-CC	60
 QY	 431	 GGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGTGTA	 490
Db	61	GGCCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA	120
 QY	 491	 AGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCCTACCGTTGGTTCAAGGATGGCAAGG	 550
Db	121	AGTGTGAGGCAGCGGCGGGAAACCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG	180
 QY	 551	 AGCTCAACCGCAGCCGAGACATT CGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC	 610
Db	181	AACTCAACCGGAGTCGTGATATT CGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC	240
 QY	 611	 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA	 670
Db	241	TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA	300
 QY	 671	 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT	 730

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      |||| ||||| ||||| || || ||||| ||||| ||||| |||||
Db      301 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCCTCTGT 360
QY      731 CATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
      ||||| ||||| || ||||| ||||| ||||| ||||| || || |||||
Db      361 CATCCTGGTCGGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 420
QY      791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCTGTGGGAT 850
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      421 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 480
QY      851 ACACCGGGGACAGGTGTCAGCAG 873
      | ||| | || ||| |||
Db      481 TCTTCGGACAGAGATGTTTGGAG 503

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Job time : 433.237 secs

OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 05:20:54 ; Search time 82.0629 Seconds
(without alignments)
6065.966 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggcccc.....caatggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	835.4	93.1	1884	3	US-08-753-007A-5	Sequence 5, Appli
2	835.4	93.1	1884	3	US-09-398-496-5	Sequence 5, Appli
3	784	87.4	3441	2	US-08-525-864A-1	Sequence 1, Appli
4	738.6	82.3	993	2	US-08-525-864A-3	Sequence 3, Appli
5	427.8	47.7	1476	3	US-08-753-007A-7	Sequence 7, Appli
6	427.8	47.7	1476	3	US-09-398-496-7	Sequence 7, Appli
7	427.8	47.7	2268	3	US-08-753-007A-31	Sequence 31, Appl
8	427.8	47.7	2268	3	US-09-398-496-31	Sequence 31, Appl
9	405.4	45.2	1607	3	US-08-753-007A-3	Sequence 3, Appli
10	405.4	45.2	1607	3	US-09-398-496-3	Sequence 3, Appli
11	405.4	45.2	2467	3	US-08-753-007A-1	Sequence 1, Appli

12	405.4	45.2	2467	3	US-09-398-496-1	Sequence 1, Appli
13	216.2	24.1	1207	2	US-08-525-864A-5	Sequence 5, Appli
14	84	9.4	2003	1	US-08-036-555B-21	Sequence 21, Appl
15	84	9.4	2003	1	US-08-469-569-21	Sequence 21, Appl
16	84	9.4	2003	1	US-08-249-322A-21	Sequence 21, Appl
17	84	9.4	2003	1	US-08-469-526A-21	Sequence 21, Appl
18	84	9.4	2003	2	US-08-734-591A-21	Sequence 21, Appl
19	84	9.4	2003	2	US-08-469-660-21	Sequence 21, Appl
20	84	9.4	2003	3	US-08-341-018-71	Sequence 71, Appl
21	84	9.4	2003	3	US-08-470-335-21	Sequence 21, Appl
22	84	9.4	2003	3	US-08-735-021-21	Sequence 21, Appl
23	84	9.4	2003	3	US-08-734-664A-21	Sequence 21, Appl
24	84	9.4	2003	3	US-08-470-339-21	Sequence 21, Appl
25	84	9.4	2003	4	US-08-467-602-21	Sequence 21, Appl
26	84	9.4	2003	5	PCT-US94-05083C-21	Sequence 21, Appl
27	84	9.4	2003	5	PCT-US95-06846A-21	Sequence 21, Appl
28	83.4	9.3	1108	1	US-08-036-555B-135	Sequence 135, App
29	83.4	9.3	1108	1	US-08-469-569-135	Sequence 135, App
30	83.4	9.3	1108	1	US-08-249-322A-135	Sequence 135, App
31	83.4	9.3	1108	1	US-08-469-526A-135	Sequence 135, App
32	83.4	9.3	1108	2	US-08-734-591A-135	Sequence 135, App
33	83.4	9.3	1108	2	US-08-469-660-135	Sequence 135, App
34	83.4	9.3	1108	3	US-08-341-018-5	Sequence 5, Appli
35	83.4	9.3	1108	3	US-08-470-335-135	Sequence 135, App
36	83.4	9.3	1108	3	US-08-735-021-135	Sequence 135, App
37	83.4	9.3	1108	3	US-08-734-664A-135	Sequence 135, App
38	83.4	9.3	1108	3	US-08-470-339-135	Sequence 135, App
39	83.4	9.3	1108	4	US-08-467-602-135	Sequence 135, App
40	83.4	9.3	1108	5	PCT-US94-05083C-131	Sequence 131, App
41	83.4	9.3	1108	5	PCT-US95-06846A-135	Sequence 135, App
42	78.4	8.7	1193	1	US-08-469-526A-134	Sequence 134, App
43	78.4	8.7	1193	2	US-08-734-591A-134	Sequence 134, App
44	78.4	8.7	1193	3	US-08-341-018-3	Sequence 3, Appli
45	78.4	8.7	1193	3	US-08-470-335-134	Sequence 134, App

ALIGNMENTS

RESULT 1

US-08-753-007A-5

; Sequence 5, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,007A
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1884 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 664...1883
; OTHER INFORMATION:
US-08-753-007A-5

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Query Match          93.1%; Score 835.4; DB 3; Length 1884;
Best Local Similarity 98.1%; Pred. No. 2.3e-201;
Matches 856; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
        |||
Db      218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 277

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db      278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db      338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db      398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db      458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517

Qy      301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

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      |||
Db      518 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
      |||
Db      578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636
Qy      421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
      |||
Db      637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696
Qy      481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
      |||
Db      697 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
Qy      541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
      |||
Db      757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 816
Qy      601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
      |||
Db      817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
Qy      661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
      |||
Db      877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
Qy      721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
      |||
Db      937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
Qy      781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
      |||
Db      997 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
Qy      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
      ||
Db      1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

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RESULT 2

US-09-398-496-5

; Sequence 5, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

```

;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/398,496
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/753,007
;   FILING DATE:  19-NOV-1996
;   APPLICATION NUMBER:  08/699,591
;   FILING DATE:  19-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Fasse, J. Peter
;   REGISTRATION NUMBER:  32,983
;   REFERENCE/DOCKET NUMBER:  07334/022001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-542-5070
;   TELEFAX:  617-542-8906
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  5:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1884 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;   NAME/KEY:  Coding Sequence
;   LOCATION:  664...1883
;   OTHER INFORMATION:
US-09-398-496-5

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Query Match          93.1%;  Score 835.4;  DB 3;  Length 1884;
Best Local Similarity 98.1%;  Pred. No. 2.3e-201;
Matches 856;  Conservative 0;  Mismatches 16;  Indels 1;  Gaps 1;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
      |||
Db     218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 277
      |||

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db     278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337
      |||

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
Db     338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397
      |||

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
      |||
Db     398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457
      |||

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
Qy      301 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db      518 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          |||
Db      578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636
Qy      421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
          |||
Db      637 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696
Qy      481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
          |||
Db      697 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
Qy      541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
          |||
Db      757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 816
Qy      601 AACTCAGACTACAGTTCAACAAGGTGAAGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
          |||
Db      817 AACTCAGACTACAGTTCAACAAGGTGAAGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
Qy      661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
          |||
Db      877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
Qy      721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
          |||
Db      937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
Qy      781 TCGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
          |||
Db      997 TCGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
Qy      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873
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Db      1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 1089

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RESULT 3

US-08-525-864A-1

; Sequence 1, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses

; TITLE OF INVENTION: Related thereto

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts


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; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,864A
; FILING DATE: 8-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3441 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 180..2441
US-08-525-864A-1

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Query Match          87.4%; Score 784; DB 2; Length 3441;
Best Local Similarity 92.2%; Pred. No. 2.5e-188;
Matches 826; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      180 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239
        |||

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db      240 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299
        |||

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db      300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 359
        |||

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db      360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419
        |||

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db      420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
        |||

Qy      301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||
Db      480 CGCTACATCTTTTTCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 539
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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  AscII (text)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/525,864A
;   FILING DATE:  8-SEP-1995
;   CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Kara, Catherine J.
;   REGISTRATION NUMBER:  41,106
;   REFERENCE/DOCKET NUMBER:  HUI-017
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617)227-7400
;   TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  993 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  1..990
US-08-525-864A-3

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Query Match          82.3%;  Score 738.6;  DB 2;  Length 993;
Best Local Similarity  90.4%;  Pred. No. 4.7e-177;
Matches 789;  Conservative  0;  Mismatches  84;  Indels  0;  Gaps  0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
        |||
Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 60

Qy     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db     61 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db    121 GGCAAGGTACAGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCT 180

Qy    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db    181 CCCGCCTCGGGTCGGGTGGCGTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 300

Qy    301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||
Db    301 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 360

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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Db    361 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

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QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
 |||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 QY 843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
 |||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

RESULT 6

US-09-398-496-7

; Sequence 7, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/398,496

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/753,007

; FILING DATE: 19-NOV-1996

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1476 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

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;      NAME/KEY:  Coding Sequence
;      LOCATION:  69...1475
;      OTHER INFORMATION:
US-09-398-496-7

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Query Match 47.7%; Score 427.8; DB 3; Length 1476;
Best Local Similarity 89.8%; Pred. No. 1.3e-98;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGCAAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCAGTACTG	422
Db	98	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCAGGGGAGAA	157
Qy	423	CGCCACCCGGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTAAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTAAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723	CACCCTGTGCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCCTATTG	782
Db	458	CACCCTGTGCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCCTATTG	517
Qy	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC	842
Db	518	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAAATGTCC	577
Qy	843	TGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	578	AAATGGATTCTTCGGACAGAGATGTTTGGAG	608

RESULT 7

US-08-753-007A-31

; Sequence 31, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

```

;   ADDRESSEE:  Fish & Richardson P.C.
;   STREET:    225 Franklin Street
;   CITY:     Boston
;   STATE:    MA
;   COUNTRY:   US
;   ZIP:      02110-2804
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:   IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:   FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/753,007A
;   FILING DATE:   19-NOV-1996
;   CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/699,591
;   FILING DATE:   19-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:         Fasse, J. Peter
;   REGISTRATION NUMBER:  32,983
;   REFERENCE/DOCKET NUMBER:  07334/022001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:    617-542-5070
;   TELEFAX:     617-542-8906
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  31:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:      2268 base pairs
;   TYPE:        nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:    linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;   NAME/KEY:     Coding Sequence
;   LOCATION:     69...2009
;   OTHER INFORMATION:
US-08-753-007A-31

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Query Match          47.7%;  Score 427.8;  DB 3;  Length 2268;
Best Local Similarity 89.8%;  Pred. No. 1.5e-98;
Matches 459;  Conservative 0;  Mismatches 52;  Indels 0;  Gaps 0;

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Qy      363 CCTCGATACCAACGGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | | | | | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      ||||| | | | | | | | | | | | | | | | | |
Db      158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      ||||| | | | | | | | | | | | | | | | | |
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAGAA 602
      ||||| | | | | | | | | | | | | | | | | |

```



```

; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...2009
; OTHER INFORMATION:
US-09-398-496-31

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Query Match          47.7%; Score 427.8; DB 3; Length 2268;
Best Local Similarity 89.8%; Pred. No. 1.5e-98;
Matches 459; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
        || || | || | | | | | | | | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
        |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
        |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
        |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
        |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
        |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
        |||||
Db      458 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
        |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAATGTCC 577

Qy      843 TGTGGGATACACCGGGGACAGGTGTGAGCAG 873
        |||| | || | || | || |
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

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RESULT 9
 US-08-753-007A-3
 ; Sequence 3, Application US/08753007A
 ; Patent No. 6074841
 ; GENERAL INFORMATION:
 ; APPLICANT: Gearing, David P.
 ; APPLICANT: Busfield, Samantha J.
 ; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/753,007A
 ; FILING DATE: 19-NOV-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/699,591
 ; FILING DATE: 19-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07334/022001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1607 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 79...621
 ; OTHER INFORMATION:
 US-08-753-007A-3

Query Match 45.2%; Score 405.4; DB 3; Length 1607;
 Best Local Similarity 87.9%; Pred. No. 5.8e-93;
 Matches 442; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430

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      | |||||
Db      2 CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

Qy      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
      | |||||
Db      62 GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

Qy      491 AGTGTGAGGCAGCAGCCGGAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
      | |||||
Db      122 AGTGTGAGGCAGCGCGGGAAACCCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181

Qy      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
      | |||||
Db      182 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC 241

Qy      611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
      | |||||
Db      242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301

Qy      671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
      | |||||
Db      302 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCACCTCTGT 361

Qy      731 CATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
      | |||||
Db      362 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421

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Db      482 TCTTCGGACAGAGATGTTTGGAG 504

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RESULT 10

US-09-398-496-3

; Sequence 3, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

US-08-753-007A-1

Matches 442; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Db 482 TCTTCGGACAGAGATGTTTGGAG 504

US-09-398-496-1

; Patent No. 6133423

APPLICANT: Gearing, David P.

10; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

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; TITLE OF INVENTION:  AND USES THEREFOR
; NUMBER OF SEQUENCES:  33
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Fish & Richardson P.C.
;   STREET:  225 Franklin Street
;   CITY:  Boston
;   STATE:  MA
;   COUNTRY:  US
;   ZIP:  02110-2804
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/398,496
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/753,007
;   FILING DATE:  19-NOV-1996
;   APPLICATION NUMBER:  08/699,591
;   FILING DATE:  19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Fasse, J. Peter
;   REGISTRATION NUMBER:  32,983
;   REFERENCE/DOCKET NUMBER:  07334/022001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-542-5070
;   TELEFAX:  617-542-8906
;   TELEX:
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  2467 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  circular
; MOLECULE TYPE:  cDNA
; FEATURE:
;   NAME/KEY:  Coding Sequence
;   LOCATION:  79...1893
;   OTHER INFORMATION:
US-09-398-496-1

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Query Match          45.2%;  Score 405.4;  DB 3;  Length 2467;
Best Local Similarity 87.9%;  Pred. No. 6.7e-93;
Matches 442;  Conservative 0;  Mismatches 61;  Indels 0;  Gaps 0;

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QY      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
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QY      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
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Db      62 GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

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Db      122 AGTGTGAGGCAGCGCGGGAAACCCCGAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181
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Qy      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
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Db      182 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC 241
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Qy      611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
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Qy      671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
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Qy      791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCCTGTGGGAT 850
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Db      422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 481
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RESULT 13

US-08-525-864A-5

; Sequence 5, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses

; TITLE OF INVENTION: Related thereto

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: AscII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/525,864A

; FILING DATE: 8-SEP-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kara, Catherine J.

; REGISTRATION NUMBER: 41,106

; REFERENCE/DOCKET NUMBER: HUI-017

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..394
US-08-525-864A-5

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Best Local Similarity 86.3%; Pred. No. 2.7e-45;
Matches 239; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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RESULT 14

US-08-036-555B-21

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; Sequence 21, Application US/08036555B
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; Patent No. 5530109

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

7
; TITLE OF INVENTION: Preparation and Use

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

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; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: N in positions 31 and 32 could be either
; OTHER INFORMATION: A or G.
US-08-036-555B-21

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QY      249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACAT 308
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;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
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;      COMPUTER:  IBM
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;      APPLICATION NUMBER:  08/036,555
;      FILING DATE:  24-MAR-1993
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
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;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
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;      PRIOR APPLICATION DATA:
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;      FILING DATE:  10-APRIL-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 5250.4
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;      INFORMATION FOR SEQ ID NO: 21:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  2003
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;      STRANDEDNESS:  single
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US-08-469-569-21

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Best Local Similarity 49.0%;  Pred. No. 6.9e-12;
Matches 361;  Conservative 0;  Mismatches 345;  Indels 30;  Gaps 4;

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Qy      189 GGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGGGGGCTGCA 248
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Qy      249 GCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACAT 308

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OM nucleic - nucleic search, using sw model

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(without alignments)
9096.466 Million cell updates/sec

Title: US-09-864-675-3
Perfect score: 897
Sequence: 1 atgaggcgcgacccggccccc.....caatgggtcaacttctcctaa 897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result Query

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3	835.4	93.1	1884	14	US-10-096-241-5	Sequence 5, Appli
4	427.8	47.7	1476	14	US-10-096-241-7	Sequence 7, Appli
5	427.8	47.7	2268	14	US-10-096-241-31	Sequence 31, Appl
6	424.8	47.4	22693	13	US-10-271-416-6	Sequence 6, Appli
7	424	47.3	1054	16	US-10-447-839A-10	Sequence 10, Appl
8	405.4	45.2	1607	14	US-10-096-241-3	Sequence 3, Appli
9	405.4	45.2	2467	14	US-10-096-241-1	Sequence 1, Appli
10	173	19.3	201	15	US-10-029-386-26613	Sequence 26613, A
11	173	19.3	419	16	US-10-447-839A-11	Sequence 11, Appl
12	173	19.3	573	15	US-10-029-386-12913	Sequence 12913, A
13	173	19.3	45450	13	US-10-271-416-7	Sequence 7, Appli
14	124.6	13.9	493	16	US-10-447-839A-12	Sequence 12, Appl
15	124	13.8	350	16	US-10-447-839A-13	Sequence 13, Appl
c 16	113.6	12.7	579	15	US-10-029-386-2532	Sequence 2532, Ap
c 17	111.8	12.5	171	15	US-10-029-386-16232	Sequence 16232, A
18	84	9.4	1986	10	US-09-373-658-71	Sequence 71, Appl
19	84	9.4	1986	11	US-09-989-687-71	Sequence 71, Appl
20	84	9.4	2003	8	US-08-736-019-21	Sequence 21, Appl
21	84	9.4	2003	10	US-09-366-886-71	Sequence 71, Appl
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23	84	9.4	2003	11	US-09-989-687-72	Sequence 72, Appl
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25	83.4	9.3	1108	10	US-09-366-886-5	Sequence 5, Appli
26	78.4	8.7	1193	8	US-08-736-019-134	Sequence 134, App
27	78.4	8.7	1193	10	US-09-366-886-3	Sequence 3, Appli
28	76.8	8.6	1140	8	US-08-736-019-149	Sequence 149, App
29	76.8	8.6	1140	10	US-09-366-886-55	Sequence 55, Appl
30	72.8	8.1	744	8	US-08-736-019-133	Sequence 133, App
31	72.8	8.1	744	10	US-09-366-886-1	Sequence 1, Appli
32	58.8	6.6	310	16	US-10-447-839A-15	Sequence 15, Appl
33	58.8	6.6	848	13	US-10-027-632-158930	Sequence 158930,
34	58.8	6.6	848	16	US-10-027-632-158930	Sequence 158930,
35	54.6	6.1	3272	12	US-10-152-319A-1922	Sequence 1922, Ap
36	52	5.8	1092	15	US-10-156-761-4747	Sequence 4747, Ap
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38	51	5.7	162	15	US-10-076-816-8	Sequence 8, Appli
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41	50.6	5.6	3111	9	US-09-773-517-12	Sequence 12, Appl
42	50.6	5.6	3111	9	US-09-792-025-12	Sequence 12, Appl
43	50.6	5.6	3111	9	US-09-849-868-12	Sequence 12, Appl
44	50.6	5.6	3111	15	US-10-290-578-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-09-864-675-3

; Sequence 3, Application US/09864675

; Patent No. US20020081286A1

; GENERAL INFORMATION:

; APPLICANT: Marchionni, Mark
; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
; FILE REFERENCE: 04585/049002
; CURRENT APPLICATION NUMBER: US/09/864,675
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,495
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-675-3

Query Match 100.0%; Score 897; DB 9; Length 897;
Best Local Similarity 100.0%; Pred. No. 2.2e-244;
Matches 897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTTCAAG	540
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      |||
Db      781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
Qy      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA 897
      |||
Db      841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTCCTAA 897

```

RESULT 2

US-09-864-675-1

; Sequence 1, Application US/09864675

; Patent No. US20020081286A1

; GENERAL INFORMATION:

; APPLICANT: Marchionni, Mark

; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,

; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS

; FILE REFERENCE: 04585/049002

; CURRENT APPLICATION NUMBER: US/09/864,675

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/206,495

; PRIOR FILING DATE: 2000-05-23

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 994

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-864-675-1

Query Match 94.6%; Score 849; DB 9; Length 994;

Best Local Similarity 98.3%; Pred. No. 9.7e-231;

Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
      |||
Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

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```

; GENERAL INFORMATION:
;   APPLICANT: Gearing, David P.
;               Busfield, Samantha J.
;   TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
;                       AND USES THEREFOR
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Fish & Richardson P.C.
;       STREET: 225 Franklin Street
;       CITY: Boston
;       STATE: MA
;       COUNTRY: US
;       ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/096,241
;       FILING DATE: 12-Mar-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/699,591
;       FILING DATE: 19-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Fasse, J. Peter
;       REGISTRATION NUMBER: 32,983
;       REFERENCE/DOCKET NUMBER: 07334/022001
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 617-542-5070
;       TELEFAX: 617-542-8906
;       TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1884 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY: Coding Sequence
;           LOCATION: 664...1883
;       OTHER INFORMATION:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-096-241-5

```

```

Query Match          93.1%;  Score 835.4;  DB 14;  Length 1884;
Best Local Similarity 98.1%;  Pred. No. 8.2e-227;
Matches 856;  Conservative 0;  Mismatches 16;  Indels 1;  Gaps 1;

```

```

Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
        |||
Db      218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277
        |||

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||

```

Db	278	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	337
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAAG	600
Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAAG	816
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937	ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	840
Db	997	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT	1056
Qy	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	1057	CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	1089

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; Sequence 7, Application US/10096241
; Publication No. US20020127594A1
;   GENERAL INFORMATION:
;     APPLICANT: Gearing, David P.
;               Busfield, Samantha J.
;     TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
;                       AND USES THEREFOR
;     NUMBER OF SEQUENCES: 33
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Fish & Richardson P.C.
;       STREET: 225 Franklin Street
;       CITY: Boston
;       STATE: MA
;       COUNTRY: US
;       ZIP: 02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/096,241
;       FILING DATE: 12-Mar-2002
;       CLASSIFICATION: <Unknown>
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/699,591
;       FILING DATE: 19-AUG-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Fasse, J. Peter
;       REGISTRATION NUMBER: 32,983
;       REFERENCE/DOCKET NUMBER: 07334/022001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 617-542-5070
;       TELEFAX: 617-542-8906
;       TELEX: <Unknown>
;     INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 1476 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;         NAME/KEY: Coding Sequence
;         LOCATION: 69...1475
;         OTHER INFORMATION:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-096-241-7

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Query Match          47.7%;  Score 427.8;  DB 14;  Length 1476;
Best Local Similarity 89.8%;  Pred. No. 3.9e-111;
Matches 459;  Conservative 0;  Mismatches 52;  Indels 0;  Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
        || || | || | | | | || | || | | | | |
Db      98  CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

```

Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723	CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTATTG	782
Db	458	CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTATTG	517
Qy	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC	842
Db	518	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAAATGTCC	577
Qy	843	TGTGGGATACACCGGGGACAGGTGTCAGCAG	873
Db	578	AAATGGATTCTTCGGACAGAGATGTTTGAG	608

RESULT 5

US-10-096-241-31

; Sequence 31, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

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;          FILING DATE: 12-Mar-2002
;          CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/699,591
;          FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
;          NAME: Fasse, J. Peter
;          REGISTRATION NUMBER: 32,983
;          REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 617-542-5070
;          TELEFAX: 617-542-8906
;          TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 31:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 2268 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: Coding Sequence
;   LOCATION: 69...2009
;   OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-096-241-31

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Query Match          47.7%;  Score 427.8;  DB 14;  Length 2268;
Best Local Similarity 89.8%;  Pred. No. 4.3e-111;
Matches 459;  Conservative 0;  Mismatches 52;  Indels 0;  Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      98  CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```

Db      458 CACCCTGTCATCCTGGTCGGGGACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
QY      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGTCC 842
        |||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
QY      843 TGTGGGATACACCGGGGACAGGTGTCAGCAG 873
        |||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAG 608

```

RESULT 6

US-10-271-416-6

```

; Sequence 6, Application US/10271416
; Publication No. US20040043021A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22693
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-6

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Query Match          47.4%; Score 424.8; DB 13; Length 22693;
Best Local Similarity 94.2%; Pred. No. 5.3e-110;
Matches 452; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

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QY      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
        |||
Db      20809 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 20868
QY      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db      20869 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 20928
QY      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db      20929 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 20988
QY      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db      20989 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 21048

```

```

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db      21049 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 21108

Qy      301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db      21109 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 21168

Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          |||
Db      21169 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 21228

Qy      421 TGC-GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAA 479
          ||| | | || || | | | | | ||| ||| |||
Db      21229 TGCGGTGAGTCGCCCCCTCCCTTTGCTGGAGAAAGGGGGGAGGGGCGAGGTGGTGGAGAA 21288

```

RESULT 7

US-10-447-839A-10

; Sequence 10, Application US/10447839A

; Publication No. US20040018181A1

; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.

; APPLICANT: Kharbanda, Surender

; APPLICANT: Weitman, Steven D.

; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM

; FILE REFERENCE: 1000.05.009

; CURRENT APPLICATION NUMBER: US/10/447,839A

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: 10/293,391

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/951,938

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: 60/231,841

; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 1054

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-447-839A-10

Query Match 47.3%; Score 424; DB 16; Length 1054;

Best Local Similarity 100.0%; Pred. No. 4.3e-110;

Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
          |||
Db      589 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 648

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          |||
Db      649 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 708

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180

```

Db	709	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	768
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	769	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	828
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	829	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	888
Qy	301	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	889	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	948
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	949	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	1008
Qy	421	TGCG	424
Db	1009	TGCG	1012

RESULT 8

US-10-096-241-3

; Sequence 3, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 79...621
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-096-241-3

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RESULT 9
 US-10-096-241-1
 ; Sequence 1, Application US/10096241
 ; Publication No. US20020127594A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gearing, David P.
 ; Busfield, Samantha J.
 ; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
 ; AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/096,241
 ; FILING DATE: 12-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/699,591
 ; FILING DATE: 19-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 07334/022001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2467 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 79...1893
 ; OTHER INFORMATION:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-096-241-1

Query Match 45.2%; Score 405.4; DB 14; Length 2467;
 Best Local Similarity 87.9%; Pred. No. 1e-104;
 Matches 442; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

; ORGANISM: Homo sapiens

```
; FEATURE:
; OTHER INFORMATION: MAP TO CHR5.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66
; OTHER INFORMATION: SWISSPROT HIT: O14511, EVALUE 3.00e-29
; OTHER INFORMATION: NT HIT: AF119152.1, EVALUE 1.00e-109
; OTHER INFORMATION: EST_HUMAN HIT: BF108794.1, EVALUE 3.00e-93
US-10-029-386-26613
```

```
Query Match          19.3%; Score 173; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.1e-39;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
          |||
Db      27  GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 86

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
          |||
Db      87  TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 146

Qy      544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 596
          |||
Db      147 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 199
```

RESULT 11

```
US-10-447-839A-11
; Sequence 11, Application US/10447839A
; Publication No. US20040018181A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbanda, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-447-839A-11
```

```
Query Match          19.3%; Score 173; DB 16; Length 419;
Best Local Similarity 100.0%; Pred. No. 6.1e-39;
```

```

Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
      |||
Db       50 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 109

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
      |||
Db      110 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 169

Qy      544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 596
      |||
Db      170 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 222

```

RESULT 12

US-10-029-386-12913

; Sequence 12913, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE

; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 12913

; LENGTH: 573

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR5.3

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.55

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.66

; OTHER INFORMATION: SWISSPROT HIT: O14511, EVALUE 2.00e-28

; OTHER INFORMATION: NT HIT: AF119152.1, EVALUE 0.00e+00

; OTHER INFORMATION: EST_HUMAN HIT: BG996653.1, EVALUE 1.00e-108

US-10-029-386-12913

```

Query Match          19.3%; Score 173; DB 15; Length 573;
Best Local Similarity 100.0%; Pred. No. 6.6e-39;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
      |||
Db      377 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 436

Qy      484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
      |||
Db      437 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 496

```


Qy 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAG 596
 |||
 Db 497 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAG 549

RESULT 13

US-10-271-416-7

; Sequence 7, Application US/10271416
 ; Publication No. US20040043021A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith, Tim
 ; APPLICANT: Little, Randall D.
 ; APPLICANT: Van Eerdewegh, Paul
 ; APPLICANT: Dupuis, Josee
 ; APPLICANT: Del Mastro, Richard G.
 ; APPLICANT: Allen, Kristina
 ; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
 ; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
 ; FILE REFERENCE: 2976-4045
 ; CURRENT APPLICATION NUMBER: US/10/271,416
 ; CURRENT FILING DATE: 2002-10-11
 ; PRIOR APPLICATION NUMBER: 60/328,424
 ; PRIOR FILING DATE: 2001-10-11
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 45450
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(45450)
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-271-416-7

Query Match 19.3%; Score 173; DB 13; Length 45450;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
 |||
 Db 7026 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 7085
 Qy 484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
 |||
 Db 7086 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 7145
 Qy 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAG 596
 |||
 Db 7146 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAG 7198

RESULT 14

US-10-447-839A-12

; Sequence 12, Application US/10447839A
 ; Publication No. US20040018181A1

```

; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbanda, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED
THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-447-839A-12

```

```

Query Match          13.9%; Score 124.6; DB 16; Length 493;
Best Local Similarity 93.5%; Pred. No. 3.5e-25;
Matches 130; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy      594 CAGAAAGAACTCACGACTACAGTTCACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
          |||
Db      227 CAGAAAGAACTCACGACTACAGTTCACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 286
          |||

Qy      654 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 713
          |||
Db      287 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 346
          |||

Qy      714 CGTGAGCACCACCCTGTCA 732
          || || || | ||
Db      347 CGGTAGGTGGGCCAGACA 365

```

RESULT 15

US-10-447-839A-13

```

; Sequence 13, Application US/10447839A
; Publication No. US20040018181A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbanda, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED
THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11

```

; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-447-839A-13

Query Match 13.8%; Score 124; DB 16; Length 350;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      715 GTGAGCACCACCCTGTCATCCTGGTCGGGGGCACGCCC GGAAGTGCAACGAGACAGCCAAG 774
          |||
Db      99 GTGAGCACCACCCTGTCATCCTGGTCGGGGGCACGCCC GGAAGTGCAACGAGACAGCCAAG 158

Qy      775 TCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGC 834
          |||
Db     159 TCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGC 218

Qy      835 AAGT 838
          |||
Db     219 AAGT 222
```

Search completed: August 15, 2004, 12:23:39
Job time : 491.839 secs